

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 20, 2005, 10:34:32 ; Search time 12 Seconds  
(without alignments)  
79.718 Million cell updates/sec

US-10-618-797-2

Title:

Perfect score: 803

Sequence:

1 MRSCPBEQYWAALLGTMCFC.....FPQLPPTQLSLGPNIGGLL 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 51470 seqs, 6736768 residues

Total number of hits satisfying chosen parameters: 51470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA New:\*
- 1: /cgn2\_6/ptodata/1/pubpaa/US09 NEW PUB.pep:\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/US06 NEW PUB.pep:\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US07 NEW PUB.pep:\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US08 NEW PUB.pep:\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/PCT NEW PUB.pep:\*
  - 6: /cgn2\_6/ptodata/1/pubpaa/US10 NEW PUB.pep:\*
  - 7: /cgn2\_6/ptodata/1/pubpaa/US11 NEW PUB.pep:\*
  - 8: /cgn2\_6/ptodata/1/pubpaa/US60 NEW PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	199.5	24.8	292	6	US-10-967-527A-19
2	195	24.3	293	6	US-10-742-634-7
3	180	22.4	293	6	US-10-967-527A-20
4	107.5	13.4	249	6	US-10-967-527A-21
5	77	9.6	1005	7	US-11-113-424-63
6	76.5	9.5	833	7	US-11-076-187-5
7	73	9.1	260	7	US-11-182-946-8
8	71	8.8	164	6	US-10-131-826A-314
9	70	8.7	3002	6	US-10-821-234-916
10	68	8.5	451	7	US-10-102-240-82
11	67	8.3	504	6	US-10-999-782-2
12	66.5	8.3	283	6	US-10-987-663-4
13	66	8.2	235	7	US-11-126-126-16
14	66	8.2	461	7	US-11-132-285-6
15	65	8.2	461	7	US-11-182-946-4
16	65	8.1	1213	7	US-11-039-398-14
17	65	8.1	1219	7	US-11-039-398-10
18	65	8.1	1232	7	US-11-039-398-18
19	65	8.1	1249	7	US-11-039-398-22
20	64	8.0	172	6	US-10-821-234-1272
21	64	8.0	4555	6	US-10-995-561-556
22	63.5	7.9	237	6	US-10-967-527A-17
23	63.5	7.9	816	7	US-11-090-439-48
24	63.5	7.9	1036	6	US-10-131-826A-142
25	63	7.8	2764	6	US-10-995-561-691

26	63	7.8	2813	6	US-10-995-561-688	Sequence 688, App
27	63	7.8	2919	6	US-10-821-234-1133	Sequence 1133, Ap
28	63	7.8	5179	7	US-11-108-172-1068	Sequence 1068, Ap
29	62.5	7.8	184	6	US-10-742-634-9	Sequence 9, Appli
30	62.5	7.8	184	6	US-10-967-527A-8	Sequence 8, Appli
31	62	7.7	838	6	US-10-645-441-9	Sequence 9, Appli
32	62	7.7	997	7	US-11-113-424-37	Sequence 37, Appl
33	62	7.7	4419	6	US-10-821-234-1155	Sequence 1155, Ap
34	62	7.7	5405	7	US-11-108-172-1119	Sequence 1119, Ap
35	61.5	7.7	504	6	US-10-821-234-1119	Sequence 1119, Ap
36	61.5	7.7	504	6	US-10-763-712A-78	Sequence 78, Appl
37	61	7.6	755	7	US-11-067-121-6	Sequence 6, Appli
38	61	7.6	843	6	US-10-645-441-7	Sequence 7, Appli
39	61	7.6	843	6	US-10-645-441-8	Sequence 8, Appli
40	60.5	7.5	126	7	US-11-113-424-184	Sequence 184, App
41	60.5	7.5	349	7	US-11-182-946-13	Sequence 13, Appl
42	60.5	7.5	598	7	US-11-082-389-398	Sequence 398, App
43	60.5	7.5	783	7	US-11-186-284-59	Sequence 59, Appl
44	60.5	7.5	3690	6	US-10-995-561-1016	Sequence 1016, Ap
45	60.5	7.5	3714	6	US-10-995-561-1015	Sequence 1015, Ap

ALIGNMENTS

RESULT 1  
US-10-967-527A-19  
; Sequence 19, Application US/10967527A  
; Publication No. US20050256041A1  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Brian A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor  
; TITLE OF INVENTION: Receptor  
; FILE REFERENCE: 03-17  
; CURRENT APPLICATION NUMBER: US/10/967,527A  
; CURRENT FILING DATE: 2004-10-18  
; PRIOR APPLICATION NUMBER: 60/511,698  
; PRIOR FILING DATE: 2003-10-16  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 292  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-967-527A-19

Query Match	24.8%	Score	199.5	DB	6	Length	292
Best Local Similarity	27.1%	Pred. No.	6.6e-13				
Matches	62	Conservative	10	Mismatches	52	Indels	105
		Gaps	6				
QY	1	MRSCPBEQYWAALLGTMCFC	AI	CN	HQS	ORT	CAASC-----GEFWDLSFGDSVITP 51
Db	31	MRSCPBEQYWDPLLTGTCMSCKT	CN	HQS	ORT	CAAF	CRSLSCRKEQKGYDHLRLDCISA 90
QY	52	NACPOS-----TLWPHSQVAER	MAGG	DVQ-----			76
Db	91	SICGQHPKQCAVPCENKLR	SPV	NLP	PELR-----		
QY	77	-----CGTSYFSTFLLWPH	CLLS	SV	NMPC	SSL	PRVL-----107
Db	147	SPALPGLKLSADQVALVYST	GLCL	CAV	LCCL	FLV	AVACFLKRGDPCSCQPRSRPQSPA 206
QY	108	-----CTCCSRCL	ECML	SI	IF	PQ	LPTQLSLGLP 136
Db	207	KSSQDHAMEAGSPVSTSP	BP	VET	CFC-----		FFCRAPTQSSAVTP 247

RESULT 2  
US-10-742-634-7  
; Sequence 7, Application US/10742634  
; Publication No. US20050249671A9

```

; GENERAL INFORMATION:
; APPLICANT: Parmelee, David
; APPLICANT: Yeh, Ren-Hwa
; APPLICANT: Galperina, Olga
; APPLICANT: Hilbert, David
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Neurokine-alpha Conjugate, Neurokine-alpha Complex, and Uses Th
; FILE REFERENCES: 1488.1810002
; CURRENT APPLICATION NUMBER: US/10/742,634
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 60/435,262
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/467,198
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-7

Query Match      24.3%; Score 195; DB 6; Length 293;
Best Local Similarity 27.0%; Pred. No. 1.8e-12;
Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

QY 1 MRSCPEQYWAALLGTCMFCKAICNHQSORTCAASC-----GEFMDLSPGDSVITP 51
DB 31 MRSCPEQYWDPLLGTCMCKTICNHQSORTCAAFCSISCRKEQKGFYDHLRLDSCA 90
QY 52 NACPQS-----TLWPHSQVAERMAGDGVQ-----
DB 91 SICGHPKQCAVFCENKLRSPVNLPPELR---RQRSGEVNNSDNGRYQGLEHRGSEA 146
QY 77 -----CGTSYPSFTLLWPHCLLSVSNMPCSSLPVL----- 107
DB 147 SPALPGLKLSAQVALVYTLGLCLCAVLCCFLVAVACFLKKGDPCCQPRSRPRQSPA 206
QY 108 -----CTCCSRCLCMLSIIIPPQL-PPTQLSLGLP 136
DB 207 KSSQDHAMEAGSPVTSPEPVEVCSPC-----PFCECAPQESAVTP 248

RESULT 3
US-10-967-527A-20
; Sequence 20, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor
; FILE REFERENCES: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 48
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(48)
; OTHER INFORMATION: cysteine rich
US-10-967-527A-20

Query Match      22.4%; Score 180; DB 6; Length 48;
Best Local Similarity 86.1%; Pred. No. 1.1e-11;
Matches 31; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

; GENERAL INFORMATION:
; APPLICANT: Parmelee, David
; APPLICANT: Yeh, Ren-Hwa
; APPLICANT: Galperina, Olga
; APPLICANT: Hilbert, David
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Neurokine-alpha Conjugate, Neurokine-alpha Complex, and Uses Th
; FILE REFERENCES: 1488.1810002
; CURRENT APPLICATION NUMBER: US/10/742,634
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 60/435,262
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/467,198
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-7

Query Match      24.3%; Score 195; DB 6; Length 293;
Best Local Similarity 27.0%; Pred. No. 1.8e-12;
Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

QY 1 MRSCPEQYWAALLGTCMFCKAICNHQSORTCAASC-----GEFMDLSPGDSVITP 51
DB 31 MRSCPEQYWDPLLGTCMCKTICNHQSORTCAAFCSISCRKEQKGFYDHLRLDSCA 90
QY 52 NACPQS-----TLWPHSQVAERMAGDGVQ-----
DB 91 SICGHPKQCAVFCENKLRSPVNLPPELR---RQRSGEVNNSDNGRYQGLEHRGSEA 146
QY 77 -----CGTSYPSFTLLWPHCLLSVSNMPCSSLPVL----- 107
DB 147 SPALPGLKLSAQVALVYTLGLCLCAVLCCFLVAVACFLKKGDPCCQPRSRPRQSPA 206
QY 108 -----CTCCSRCLCMLSIIIPPQL-PPTQLSLGLP 136
DB 207 KSSQDHAMEAGSPVTSPEPVEVCSPC-----PFCECAPQESAVTP 248

RESULT 5
US-11-113-424-63
; Sequence 63, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCES: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
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QY 1 MRSCPEQYWAALLGTCMFCKAICNHQSORTCAASC 36
DB 10 MRSCPEQYWDPLLGTCMCKTICNHQSORTCAAF 45

RESULT 4
US-10-967-527A-21
; Sequence 21, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor
; FILE REFERENCES: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 249
; TYPE: PRT
; ORGANISM: mus musculus
US-10-967-527A-21

Query Match      13.4%; Score 107.5; DB 6; Length 249;
Best Local Similarity 32.3%; Pred. No. 0.00051;
Matches 21; Conservative 10; Mismatches 25; Indels 9; Gaps 1;

QY 1 MRSCPEQYWAALLGTCMFCKAICNHQSORTCAASC-----GEFMDLSPGDSVITP 51
DB 3 MAFCPKQYWDSPKSKSCVSCALTCSORSORTCTDFCKFNCRKEQGYDHLGACVSCD 62
QY 52 NACPQ 56
DB 63 STCTQ 67

RESULT 5
US-11-113-424-63
; Sequence 63, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCES: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
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; LENGTH: 1005
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-113-424-63

Query Match          9.6%; Score 77; DB 7; Length 1005;
Best Local Similarity 26.5%; Pred. No. 1.6;
Matches 36; Conservative 7; Mismatches 61; Indels 32; Gaps 8;

QY 4 CPEQYWAALGTQMFCAICNQHOSQRTCAACGCFWDLSPGDSVITPNACQSTLWPHS 63
DB 278 CSAEGEVLPIGKCM-CKA-GYEBKNGTCQVCRGFFKASPHSQ--TCSKCP-----PHS 328
QY 64 QVAERAGAGDVQCGTGY-----PSTFLLWPHCLLSVNNPCSSLPRVLTCTCSRCLEC 117
DB 329 YTHEE--ASTSCVCEKDYFRESDPPT-----MACTRPPSAPRNAISVNE-- 372
QY 118 MLSIIPQLPPTQUSG 133
DB 373 -TSVFWLEWIPADTGG 387

RESULT 6
US-11-076-187-5
; Sequence 5, Application US/11076187
; Publication No. US20050244857A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Pan, James G
; APPLICANT: Gentz, Reiner L
; APPLICANT: Dixit, Vishva M
; TITLE OF INVENTION: Death Domain Containing Receptor-4
; FILE REFERENCE: PF359P3
; CURRENT APPLICATION NUMBER: US/11076,187
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: 60/035,722
; PRIOR FILING DATE: 1997-01-28
; PRIOR APPLICATION NUMBER: 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 09/565,918
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/406,922
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/413,861
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 10/648,786
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 60/551,768
; PRIOR FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: 60/608,469
; PRIOR FILING DATE: 2004-09-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 5
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-076-187-5

Query Match          9.5%; Score 76.5; DB 7; Length 833;
Best Local Similarity 28.1%; Pred. No. 1.5;
Matches 38; Conservative 9; Mismatches 37; Indels 51; Gaps 11;

QY 18 MFCAIC--NHQSQRTCAACGCFWDLSPGDSVITPNACQSTL--WPH----- 62
DB 462 LFCCRCGCPAGHYLKAPCTEPCGN-----STCLVCPQDTFLAWENHNSECARCOA 511
QY 63 ----SQVA-ERMAGGVDQCGTSYPSFTLLWPHCLLS--VSNMP-----CSSL---P 104
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DB 512 CDEASQVALENCASVADTRCGCK--PGMFV---ECQVSCQVSSSPFYCQPCLDGALHRRHT 567
QY 105 RVLC-----TCCSRCL 115
DB 568 RLICSRRTDTCGTCL 582

RESULT 7
US-11-182-946-8
; Sequence 8, Application US/11182946
; Publication No. US20050255100A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/11/182,946
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/186,643
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 8
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-946-8

Query Match          9.1%; Score 73; DB 7; Length 260;
Best Local Similarity 23.5%; Pred. No. 1.2;
Matches 32; Conservative 7; Mismatches 37; Indels 60; Gaps 9;

QY 2 RSCPEQYWAALGTQMFCAICNQHOSQRTCAACGCFWDLSPGDSVITPNACQSTLW 61
DB 25 KSCPERHYWAQGLKCCQMCB-----POTFLV--KDCDQ----- 55
QY 62 HSQVAERAGGVDQVC-----GTSYPSFTLLWPHCL-----LSVNNPCSSLPRVLC 108
DB 56 HRKAA-----QCDCPIPGVFSFSDHTRPHCESCRHCNSGLLVRN--CTITANAEC 104
QY 109 TC-----C--SRCLEC 117
DB 105 ACRNGWQCRDKECTEC 120

RESULT 8
US-10-131-826A-314
; Sequence 314, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Sherney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCES: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 314
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-314

Query Match      8.8%; Score 71; DB 6; Length 164;
Best Local Similarity 24.7%; Pred. No. 1.2; Mismatches 7; Indels 30; Gaps 5;
Matches 24; Conservative 7;

QY 14 LGTCMFCCKAICNHQSQRTCAASCGEFWDLSPGDSVITPNACQSTLWPHSQVAERMAAG 73
DB 67 LGAICYCDLFCN---RTVSDCCDFWDFCLG---VPPPPPP-----IQGCWHGG 109
QY 74 DVOCGTSYPSFTLWPHCHLLSVSNMPCSSLPRVLCTC 110
DB 110 RI-----YPLVGYWDNC-----NRCTC 127

RESULT 9
US-10-821-234-916
; Sequence 916, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 916
; LENGTH: 3002
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-916

Query Match      8.7%; Score 70; DB 6; Length 3002;
Best Local Similarity 22.1%; Pred. No. 20;
Matches 33; Conservative 11; Mismatches 53; Indels 52; Gaps 8;

QY 15 GTCMFCCKAICNHQSQRTCAASCGEFWD-----LSPGDSVI 49
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DB 2199 GKCSFKS--RNHSKQECCLALGEGWDPCELCPTPEAFRQICPYGSGIIVGPDSDAV 2257
QY 50 TNACQSTLWPHSQVAERMAAGDVQCGTSYPSFTLWPHCL-----LSVSNMPCSS--- 102
DB 2258 DMDCKEPPDVCKHGQCIN---TDGSYRCPCPGYT--LAGNECVDTDECSVGN--PCGNGTC 2312
QY 103 ---LPRVLCTC-----CSRCLC 117
DB 2313 KNVIGGFECTCEGPEPGPMWTCEDINEC 2341

RESULT 10
US-11-102-240-82
; Sequence 82, Application US/11102240
; Publication No. US20050260647A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESSI
; TITLE OF INVENTION: ESOPHAGEAL TUMOR
; FILE REFERENCE: P3230R1C106C
; CURRENT APPLICATION NUMBER: US/11/102,240
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 10/063662
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 199-12-09
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 82
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-102-240-82

Query Match      8.5%; Score 68; DB 7; Length 451;
Best Local Similarity 22.6%; Pred. No. 6;
Matches 38; Conservative 20; Mismatches 64; Indels 46; Gaps 9;

QY 1 MRSCPEEQYWAALL---GTCMFCCKAICNHQS-----QRTCAASCGEFWDL 42
DB 152 LTTCPEPGCPAPLPDPSCCQACKDEASEQSDSEEDSVQSLHGVHRHPQDPCSSDAGR--KR 209
QY 43 SPGDSVITPNACQSTLWPHSQ-----VAERMAAGDVQCGTSYPSFTLWPHC 91
DB 210 GGTGPTAPTGLSAPLSFIPRFRPKGAGSTTVKIVLKEKHKKACVHGKTY--SHGEVWHPA 268
QY 92 LLSVSNMPCSSLPRLVCTC-----CSRCLCMLSIIFPOLPTQLSG 133
DB 269 FRAFGPLPC-----ILCTCEDGRQDQCR-VTCPTB--YPCRHPKAVAG 308

RESULT 11
US-10-999-782-2
; Sequence 2, Application US/10999782
; Publication No. US20050266524A1
; GENERAL INFORMATION:
; APPLICANT: BULLA, Lee A.
; APPLICANT: CANDAS, Mehmet
; TITLE OF INVENTION: BETA INTEGRIN GENE AND PROTEIN
; FILE REFERENCE: 524412001100
; CURRENT APPLICATION NUMBER: US/10/999,782
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: US 60/527,072
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 2
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Manduca sexta
US-10-999-782-2

Query Match
Best Local Similarity 8.3%; Score 67; DB 6; Length 504;
Matches 30; Conservative 14; Mismatches 65; Indels 26; Gaps 5;

QY 15 GTCMFCATCNHQ-----SQRTCAASCGFWDLSPG-----DSVITPN--ACPOSTLW 60
DB 270 GVMCMGCKTCNDRSGKYCEFDKACDNLCSNHGICTLGSQCQDSGWSGNDGCGPTNTD 329
QY 61 PHSQVAEREMAG-GDVQCCTSYSPSTFLLWPHCLLSVSNMPCSSLPVLCTCCSCLCML 119
DB 330 CYAQYSEEVCSNGECVCG-----KCQAKVKGKNETYAGVFCDCNDCQSKYC 378
QY 120 SIIFPOLPPTQLSGL 134
DB 379 KALEPNVECNVIOGL 393

RESULT 12
US-10-987-663-4
; Sequence 4, Application US/10987663
; Publication No. US20050272118A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: CLARK, HILARY
; APPLICANT: EATON, DANIEL L.
; APPLICANT: WRANIK, BERND
; APPLICANT: OUYANG, WENJUN
; APPLICANT: GONZALES, LINO
; APPLICANT: LOYET, KELLY M.
; TITLE OF INVENTION: Novel Compositions and Methods for the Treatment of
; TITLE OF INVENTION: Immune Related Diseases
; FILE REFERENCE: P1996RIP1-US
; CURRENT APPLICATION NUMBER: US/10/987,663
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 60/421,236
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 10/371,341
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-987-663-4

Query Match
Best Local Similarity 8.3%; Score 66.5; DB 6; Length 283;
Matches 24; Conservative 7; Mismatches 49; Indels 15; Gaps 3;

QY 4 CPEEQYWAAL--LGTCMFCAL-----CNHQSQRTCAASCGFWDLSPGDSVIT 50
DB 78 CPPTGYIAHNLGSLKLCQMCNCDPANGLRASRNCSTENAVCGSPGHFCIVQGDHCAA 137
QY 51 PNACPOSTLWPHSQVAEREMAGDVQCCTSYSPSTF 85
DB 138 CRAVATSS--PGQVQKGTESQDTLCQNCPPGTF 170

RESULT 13
US-11-126-126-16
; Sequence 16, Application US/11126126
; Publication No. US20050250696A1
; GENERAL INFORMATION:
; APPLICANT: Fisher F., Eric
; APPLICANT: Edwards K., Carl
; APPLICANT: Kieft L., Gary

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-126-126-16

Query Match
Best Local Similarity 8.2%; Score 66; DB 7; Length 235;
Matches 30; Conservative 14; Mismatches 60; Indels 30; Gaps 6;

QY 3 SCPEBOY-----WAALLGTCMFCRA-----ICNHQSQRTCAASCGFWDLSPGDS 47
DB 55 SCEDSTYQLWNW---VPECLSCGSRSSDQVETQACTREQNRICTCRPGWYCALSKQEG 111
QY 48 VITPNAC-POSTLWPHSQVAEREMAGDVQCCTSYSPSTF-----LLWPHCLLSVSNM 98
DB 112 C---RLCAPLRKCRPGFVGARPGTETSDVCKPCAPGTFSTSTSDICRPHQICNVVAI 168
QY 99 PCSSLPVLCTCCS 112
DB 169 PGNASRDVCTSTS 182

RESULT 14
US-11-132-285-6
; Sequence 6, Application US/11132285
; Publication No. US20050244876A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR13 and TR14
; FILE REFERENCE: PFS1IPI
; CURRENT APPLICATION NUMBER: US/11/132,285
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: US/10/046,433
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/261,960
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/618,570
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/144,087
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 60/149,450
; PRIOR FILING DATE: 1999-07-18
; PRIOR APPLICATION NUMBER: 60/149,712
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/153,089
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6

```









ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER:  
APPLICATION NUMBER: US/09/782,857A  
FILING DATE: 14-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/810,572  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 1340-1-007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 293 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-782-857A-2

Query Match 24.3%; Score 195; DB 2; Length 293;  
Best Local Similarity 27.0%; Pred. No. 1.4e-11;  
Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

Qy 1 MRSCPEQYWAALGTGCMCKAICNHQSORTCAASC-----GFWDLSPGDSVITP 51  
Db 31 MRSCPEQYWDPLLTGTCMSCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90  
Qy 52 NACPQS-----TLWPHSQVAEREMAGDVQ----- 76  
Db 91 SICGHPKQCAFCENKLRSPVNLPELR-----RQRSGEVNNSDNGRYQGLEHRGSEA 146  
Qy 77 -----CGTSPSTFLLWPHCLLSVSNMPCSSLPRLV----- 107  
Db 147 SPALPGLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKRGDPCQCPQSRPRQSPA 206  
Qy 108 -----CTCCSRCLCMLSIIFPOL-PPTQLSLGLP 136  
Db 207 KSSQDHAMEAGSPVSTSPBVTETCSFC-----FPFCRAPTOESA VTP 248

RESULT 5  
US-09-879-919-22  
Sequence 22, Application US/09879919  
Patent No. 6541224  
GENERAL INFORMATION:  
APPLICANT: Yu, Guo-Liang, et al.  
TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon  
FILE REFERENCE: PF253P1  
CURRENT APPLICATION NUMBER: US/09/879,919  
CURRENT FILING DATE: 2001-06-14  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/277,978  
PRIOR FILING DATE: 2001-03-23  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/254,875  
PRIOR FILING DATE: 2000-12-13

PRIOR APPLICATION NUMBER: 60/241,952  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/211,537  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 08/815,783  
PRIOR FILING DATE: 1997-03-12  
PRIOR APPLICATION NUMBER: 60/016,812  
PRIOR FILING DATE: 1996-03-14  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 22  
LENGTH: 293  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-879-919-22

Query Match 24.3%; Score 195; DB 2; Length 293;  
Best Local Similarity 27.0%; Pred. No. 1.4e-11;  
Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

Qy 1 MRSCPEQYWAALGTGCMCKAICNHQSORTCAASC-----GFWDLSPGDSVITP 51  
Db 31 MRSCPEQYWDPLLTGTCMSCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90  
Qy 52 NACPQS-----TLWPHSQVAEREMAGDVQ----- 76  
Db 91 SICGHPKQCAFCENKLRSPVNLPELR-----RQRSGEVNNSDNGRYQGLEHRGSEA 146  
Qy 77 -----CGTSPSTFLLWPHCLLSVSNMPCSSLPRLV----- 107  
Db 147 SPALPGLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKRGDPCQCPQSRPRQSPA 206  
Qy 108 -----CTCCSRCLCMLSIIFPOL-PPTQLSLGLP 136  
Db 207 KSSQDHAMEAGSPVSTSPBVTETCSFC-----FPFCRAPTOESA VTP 248

RESULT 6  
US-09-848-295-4  
Sequence 4, Application US/09848295  
Patent No. 6623941  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Ruben, Steven M.  
TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based  
TITLE OF INVENTION: Thereon  
FILE REFERENCE: PF527  
CURRENT APPLICATION NUMBER: US/09/848,295  
CURRENT FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: 60/202,193  
PRIOR FILING DATE: 2000-05-05  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 4  
LENGTH: 293  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-848-295-4

Query Match 24.3%; Score 195; DB 2; Length 293;  
Best Local Similarity 27.0%; Pred. No. 1.4e-11;  
Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

Qy 1 MRSCPEQYWAALGTGCMCKAICNHQSORTCAASC-----GFWDLSPGDSVITP 51  
Db 31 MRSCPEQYWDPLLTGTCMSCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90  
Qy 52 NACPQS-----TLWPHSQVAEREMAGDVQ----- 76  
Db 91 SICGHPKQCAFCENKLRSPVNLPELR-----RQRSGEVNNSDNGRYQGLEHRGSEA 146  
Qy 77 -----CGTSPSTFLLWPHCLLSVSNMPCSSLPRLV----- 107

Db 147 SPALPGLKLSADQVALVYSTGLCLCAVLCCFLVAVACFLKKGDCSCQPRSRPRQSPA 206  
QY 108 -----CTCSRCLCMLSIIPQL-PPQLSGLGP 136  
Db 207 KSSQDHAMEAGSPVSTSPVETCSFC-----PPECRAPTQESAVTP 248

RESULT 7  
US-09-854-864-14  
; Sequence 14, Application US/09854864  
; Patent No. 6774106  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; FILE REFERENCE: BLYS/AGP-3, AND TACI  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; PRIOR FILING DATE: 2001-09-11  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-14

Query Match 24.3%; Score 195; DB 2; Length 293;  
Best Local Similarity 27.0%; Pred. No. 1.4e-11;  
Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

QY 1 MRSCEPYWAALLGTCMFCCKAICNHQSORTCAASC-----GEFWDLSFGDSVITP 51  
Db 31 MRSCEPYWDPLGTCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90  
QY 52 NACFQS -----TLWPHSQVAERMGADYQ----- 76  
Db 91 SICGHPKQCAYPENKLRSPVNLPELR-----QRSGEVENNSDNGRYQGLEHGRSEA 146  
QY 77 -----CGTSYSPSTFLWPHCLLSVSNMPCSSLPVYL----- 107  
Db 147 SPALPGLKLSADQVALVYSTGLCLCAVLCCFLVAVACFLKKGDCSCQPRSRPRQSPA 206  
QY 108 -----CTCSRCLCMLSIIPQL-PPQLSGLGP 136  
Db 207 KSSQDHAMEAGSPVSTSPVETCSFC-----PPECRAPTQESAVTP 248

RESULT 8  
US-08-810-572A-6  
; Sequence 6, Application US/08810572A  
; Patent No. 5969102  
; GENERAL INFORMATION:  
; APPLICANT: Bram, Richard J.  
; APPLICANT: von Bulow, Gotz  
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS  
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; FLOOR: Floor  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/290,333  
; FILING DATE: 12-Apr-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT  
; TELECOMMUNICATION INFORMATION:

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/810,572A  
; FILING DATE: 28-FEB-1997  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 1340-1-007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-487-5800  
; TELEFAX: 201-343-1684  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 166 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHEICAL: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
US-08-810-572A-6

Query Match 24.0%; Score 192.5; DB 1; Length 166;  
Best Local Similarity 56.9%; Pred. No. 1.3e-11;  
Matches 37; Conservative 4; Mismatches 15; Indels 9; Gaps 1;

QY 1 MRSCEPYWAALLGTCMFCCKAICNHQSORTCAASC-----GEFWDLSFGDSVITP 51  
Db 31 MRSCEPYWDPLGTCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90  
QY 52 NACPQ 56  
Db 91 SICGQ 95

RESULT 9  
US-09-290-333-6  
; Sequence 6, Application US/09290333  
; Patent No. 6316222  
; GENERAL INFORMATION:  
; APPLICANT: Bram, Richard J.  
; APPLICANT: von Bulow, Gotz  
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS  
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; FLOOR: Floor  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/290,333  
; FILING DATE: 12-Apr-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE: ...  
ORGANISM: Homo sapiens  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-290-333-6

Query Match 24.0%; Score 192.5; DB 2; Length 166;  
Best Local Similarity 56.9%; Pred. No. 1.3e-11;  
Matches 37; Conservative 4; Mismatches 15; Indels 9; Gaps 1;  
QY 1 MRSCPPEQYWAALLGTCMFCCKAICNHQSORTCAASC-----GEFWDLSFGDSVITP 51  
Db 31 MRSCPPEQYWDPLGTGCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90  
QY 52 NACPQ 56  
Db 91 SICGQ 95

RESULT 10  
US-09-782-857A-6  
Sequence 6, Application US/09782857A  
Patent No. 6500428  
GENERAL INFORMATION:  
APPLICANT: Bram, Richard J.  
von Bulow, Gotz  
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS  
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE  
THEREOF  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David A. Jackson, Esq.  
STREET: 411 Hackensack Ave, Continental Plaza, 4th  
Floor  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/782,857A  
FILING DATE: 14-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/810,572  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 1340-1-007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-782-857A-6  
Query Match 24.0%; Score 192.5; DB 2; Length 166;  
Best Local Similarity 56.9%; Pred. No. 1.3e-11;  
Matches 37; Conservative 4; Mismatches 15; Indels 9; Gaps 1;  
QY 1 MRSCPPEQYWAALLGTCMFCCKAICNHQSORTCAASC-----GEFWDLSFGDSVITP 51  
Db 31 MRSCPPEQYWDPLGTGCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90  
QY 52 NACPQ 56  
Db 91 SICGQ 95

RESULT 11  
US-09-854-864-15  
Sequence 15, Application US/09854864  
Patent No. 6774106  
GENERAL INFORMATION:  
APPLICANT: THEILL, LARS EYDE  
APPLICANT: YU, GANG  
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
FILE REFERENCE: A-686B  
CURRENT APPLICATION NUMBER: US/09/854,864  
CURRENT FILING DATE: 2001-09-11  
PRIOR APPLICATION NUMBER: US 60/204,039  
PRIOR FILING DATE: 2000-05-12  
PRIOR APPLICATION NUMBER: US 60/214,591  
PRIOR FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 15  
LENGTH: 166  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-854-864-15

Query Match 24.0%; Score 192.5; DB 2; Length 166;  
Best Local Similarity 56.9%; Pred. No. 1.3e-11;  
Matches 37; Conservative 4; Mismatches 15; Indels 9; Gaps 1;  
QY 1 MRSCPPEQYWAALLGTCMFCCKAICNHQSORTCAASC-----GEFWDLSFGDSVITP 51  
Db 31 MRSCPPEQYWDPLGTGCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90  
QY 52 NACPQ 56  
Db 91 SICGQ 95

RESULT 12  
US-09-854-864-18  
Sequence 18, Application US/09854864  
Patent No. 6774106  
GENERAL INFORMATION:  
APPLICANT: THEILL, LARS EYDE  
APPLICANT: YU, GANG  
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
FILE REFERENCE: A-686B  
CURRENT APPLICATION NUMBER: US/09/854,864  
CURRENT FILING DATE: 2001-09-11  
PRIOR APPLICATION NUMBER: US 60/204,039  
PRIOR FILING DATE: 2000-05-12  
PRIOR APPLICATION NUMBER: US 60/214,591

```
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-18

Query Match      24.0%; Score 192.5; DB 2; Length 397;
Best Local Similarity 56.9%; Pred. No. 3.5e-11;
Matches 37; Conservative 4; Mismatches 15; Indels 9; Gaps 1;

QY 1 MRSPCEQYWAALIGTCMFCCKAICNHQSORTCAASC-----GEFWDLSFGDSVITP 51
Db 31 MRSPCEQYWDPLIGTCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90
QY 52 NACPQ 56
Db 91 SICGQ 95

RESULT 13
US-09-854-864-16
; Sequence 16, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-16

Query Match      22.5%; Score 180.5; DB 2; Length 67;
Best Local Similarity 58.6%; Pred. No. 7.3e-11;
Matches 34; Conservative 4; Mismatches 15; Indels 5; Gaps 1;

QY 4 CPBEQYWAALIGTCMFCCKAICNHQSORTCAASC-----GEFWDLSFGDSVITPNACPQ 56
Db 1 CPBEQYWDPLIGTCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCAICQ 58

RESULT 14
US-09-854-864-20
; Sequence 20, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 20
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-20

Query Match      21.5%; Score 172.5; DB 2; Length 59;
Best Local Similarity 66.0%; Pred. No. 4e-10;
Matches 31; Conservative 2; Mismatches 5; Indels 9; Gaps 1;

QY 4 CPBEQYWAALIGTCMFCCKAICNHQSORTCAASC-----GEFWD 41
Db 1 CPBEQYWDPLIGTCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYD 47

RESULT 15
US-09-286-529-17
; Sequence 17, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-286-529-17

Query Match      11.9%; Score 95.5; DB 2; Length 299;
Best Local Similarity 25.4%; Pred. No. 0.11;
Matches 36; Conservative 9; Mismatches 46; Indels 51; Gaps 7;

QY 4 CPBE-----QYWAALLGTCMFCCKAICNHQSQ--RTCAAS-----CGEFWD 41
Db 73 CPPRHYTQFW-NYLERCRYCNVLCGEREBEARACHATHNRACRTRTGFFAHAGFCLHAS 131
QY 42 LSPGDSVITPNACPOSTLWPHSQVAERWAGDVQCGTSVPSTF-----LLWPH--- 90
Db 132 CPPGAGVIAPGTPSQNT-----QQPCPPGTFSSSSSEQCPHFNCT 174
QY 91 CLLSVSNMPCSSLPRVLCTCCS 112
Db 175 ALGLALNVFGSSSHDTLCTSCT 196

Search completed: December 20, 2005, 10:34:28
Job time : 47 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 20, 2005, 10:33:33 ; Search time 185 Seconds

(without alignments)  
337.253 Million cell updates/sec

Title: US-10-618-797-2

Perfect score: 803

Sequence: 1 MRSCPQQWAAALLGTGCMFC.....FPQLPPTQLSGLPNIGGLL 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% .....

Listing first 4% summaries

Database : A Geneseq 21:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	803	100.0	142	7	Adf77377 Human tum
2	803	100.0	142	8	Adj92512 Human TR2
3	697.5	86.9	154	5	Aae29295 Human gen
4	199.5	24.8	292	9	Adz67771 Human tum
5	198.5	24.7	291	5	Aau10949 Human AGP
6	198	24.7	293	5	Aau09900 Human AGP
7	195	24.3	265	4	Aae09244 Human TAC
8	195	24.3	266	6	Abp97723 Amino aci
9	195	24.3	266	9	Adw03442 Human TAC
10	195	24.3	293	2	Aaw75783 Human lym
11	195	24.3	293	3	Ab36312 Human neu
12	195	24.3	293	3	Aay94000 A transme
13	195	24.3	293	4	Aae09240 Human TAC
14	195	24.3	293	4	Aay71914 Human tum
15	195	24.3	293	5	Aao14130 Human tra
16	195	24.3	293	5	Abb81488 Human TAC
17	195	24.3	293	5	Aau99512 Human TAC
18	195	24.3	293	5	Aae28962 Human TAC
19	195	24.3	293	5	Aau75408 Tumour ne
20	195	24.3	293	5	Aae15493 Human tra
21	195	24.3	293	5	Abg71496 Human tum
22	195	24.3	293	6	Aae35211 Human TAC
23	195	24.3	293	6	Abp60551 Human tum
24	195	24.3	293	6	Abp97716 Amino aci

25	195	24.3	293	6	Aao29592 Human DIT
26	195	24.3	293	7	Adf72628 Human tum
27	195	24.3	293	7	Adf77379 Human tum
28	195	24.3	293	7	Abm85745 Human pro
29	195	24.3	293	8	Adk00754 Native hu
30	195	24.3	293	8	Adj92514 Human TAC
31	195	24.3	293	8	Adn03174 Human TAC
32	195	24.3	293	8	Adq76815 Human TAC
33	195	24.3	293	8	Ado94440 Neutrokin
34	195	24.3	293	9	Adw03430 Human TAC
35	195	24.3	294	9	Adw03443 Human TAC
36	195	24.3	312	5	Aao14135 Protein o
37	194	24.2	294	8	Adk00765 hTACI epl
38	193	24.0	344	6	Aae35224 Human TAC
39	192.5	24.0	166	2	Aaw75785 Human lym
40	192.5	24.0	166	5	Aae15494 Human TAC
41	192.5	24.0	171	8	Adn03188 Human TAC
42	192.5	24.0	332	6	Aae35228 Human TAC
43	192.5	24.0	348	6	Aae35225 Human TAC
44	192.5	24.0	357	6	Aae35226 Human TAC
45	192.5	24.0	366	5	Aao14132 Protein o

## ALIGNMENTS

RESULT 1

ADf77377  
ID ADf77377 standard; protein; 142 AA.

XX

AC ADf77377;

XX

DT 26-FEB-2004 (first entry)

XX

DE Human tumour necrosis factor receptor TR20.

XX

KW Human; tumour necrosis factor receptor; TR20; receptor; gene therapy;  
B cell; cell survival; upregulated cell proliferation; apoptosis; cancer;  
autoimmune disease; viral infection; inflammation;

KW graft-versus-host disease; acute graft rejection;  
chronic graft rejection; AIDS; neurodegenerative disorder;

KW myelodysplastic syndromes; ischaemic injury; toxin-induced liver disease;  
septic shock; cachexia; anorexia.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 1..142

FT Domain /note= "This region is specifically claimed in claim 39"

FT Domain /label = Extracellular domain

FT Region /note= "This region is specifically claimed in claim 39"

FT Region /note= "This region is specifically claimed in claim 1"

FT Region /note= "This region is specifically claimed in claim 1"

FT Region /note= "This region is specifically claimed in claim 1"

FT Domain /label = Intracellular domain

FT Domain /note= "This region is specifically claimed in claim 39"

XX US6623941-B1.

XX 23-SEP-2003.

PD 04-MAY-2001; 2001US-00848295.

XX 05-MAY-2000; 2000US-0202193P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Baker KP, Ni J;

PI

XX WPI; 2003-895467/82.  
 DR N-PSDB; ADF77376.  
 XX  
 XX New TR20 nucleic acid molecules, useful for treating diseases associated  
 PT with increased cell survival, upregulated cell proliferation, or  
 PT inhibition of apoptosis, e.g. cancer, autoimmune diseases, viral  
 PT infections, inflammation.  
 XX  
 XX Claim 1; SEQ ID NO 2; 102pp; English.  
 PS  
 CC The invention relates to an isolated nucleic acid molecule consisting of  
 CC a sequence that is at least 90% identical to a sequence encoding Human  
 CC tumour necrosis factor receptor (TR20) polypeptide (appearing as  
 CC ADF77377) or its fragments, complement, and optionally a heterologous  
 CC nucleic acid sequence that is preferentially expressed in mature B cells.  
 CC Also included are a method of making a recombinant vector by inserting  
 CC the nucleic acid molecule into a vector, a recombinant vector produced by  
 CC the method, a method of making a recombinant host cell by introducing the  
 CC recombinant vector into a cell, a recombinant host cell produced by the  
 CC method and a recombinant method of producing a polypeptide by culturing  
 CC the recombinant host cell under conditions where the polypeptide is  
 CC expressed and recovering the polypeptide. The nucleic acid molecules are  
 CC useful for treating diseases associated with increased cell survival,  
 CC upregulated cell proliferation, or inhibition of apoptosis, e.g. cancer,  
 CC autoimmune diseases, viral infections, inflammation, graft-versus-host  
 CC disease, acute graft rejection, chronic graft rejection, AIDS,  
 CC neurodegenerative disorders, myelodysplastic syndromes, ischaemic injury,  
 CC toxin-induced liver disease, septic shock, cachexia, and anorexia. The  
 CC present sequence represents human TR20.  
 XX  
 SQ Sequence 142 AA;  
 Query Match 100.0%; Score 803; DB 7; Length 142;  
 Best Local Similarity 100.0%; Pred. No. 3e-69;  
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRSCPEQYWAALLGTGTCFCKAICNHQSORTCAASGCEFWDLSPGDSVITPNACPOSTLW 60  
 DB 1 MRSCPEQYWAALLGTGTCFCKAICNHQSORTCAASGCEFWDLSPGDSVITPNACPOSTLW 60  
 QY 61 PHSQVAERWAGDVQCGTSYPTFTLLWPHCLLSVSNMPCSSLPVLCTCCSCLECMLS 120  
 DB 61 PHSQVAERWAGDVQCGTSYPTFTLLWPHCLLSVSNMPCSSLPVLCTCCSCLECMLS 120  
 QY 121 IIFPQLPPTQLSLGPNIGLL 142  
 DB 121 IIFPQLPPTQLSLGPNIGLL 142  
 RESULT 2  
 ADJ92512  
 ID ADJ92512 standard; protein; 142 AA.  
 XX  
 AC ADJ92512;  
 DT  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Human TR20.  
 XX human; TR20; immunodeficiency; autoimmune disease;  
 KW severe combined immunodeficiency; SCID-X linked; SCID-autosomal;  
 KW adenosine deaminase deficiency; ADA deficiency;  
 KW X-linked agammaglobulinemia; XLA; Bruton's disease;  
 KW congenital agammaglobulinemia; X-linked infantile agammaglobulinemia;  
 KW acquired agammaglobulinemia; adult onset agammaglobulinemia;  
 KW late-onset agammaglobulinemia; dysagammaglobulinemia;  
 KW hypogammaglobulinemia; transient hypogammaglobulinemia of infancy;  
 KW unspecified hypogammaglobulinemia; agammaglobulinemia;  
 KW common variable immunodeficiency; CVID; Wiskott-Aldrich Syndrome; WAS;  
 KW selective IGA deficiency; B cell lymphoproliferative disorder; BLPD;  
 KW recessive agammaglobulinemia; reticular dysgenesis;  
 KW neonatal neutropenia; severe congenital leukopenia;  
 KW thymic lymphoplasia-aplasia; ataxia-telangiectasia; XLP;  
 KW short limbed dwarfism; X-linked lymphoproliferative syndrome; XLP;  
 KW purine nucleoside phosphorylase; PNP deficiency; MHC Class II deficiency;  
 KW Bare Lymphocyte Syndrome; autoimmune haemolytic anaemia;  
 KW autoimmune neonatal thrombocytopenia;  
 KW idiopathic thrombocytopenia purpura; autoimmune thrombocytopenia;  
 KW autoimmune neutropenia; haemolytic anaemia; antiphospholipid syndrome;  
 KW dermatitis; allergic encephalomyelitis; myocarditis;  
 KW relapsing polychondritis; rheumatic heart disease; glomerulonephritis;  
 KW Multiple Sclerosis; Neuritis; Uveitis Ophthalmia; Polyendocrinopathy;  
 KW Purpura; Stiff-Man Syndrome; Autoimmune Pulmonary Inflammation;  
 KW Guillain-Barre Syndrome; insulin dependent diabetes mellitus;  
 KW juvenile onset diabetes; autoimmune thyroiditis; hypothyroidism;  
 KW receptor autoimmunity; autoimmune thrombotic purpura;  
 KW rheumatoid arthritis; gluten-sensitive enteropathy;  
 KW dense deposit disease; scleroderma; mixed connective tissue disease;  
 KW polymyositis; dermatomyositis; pernicious anaemia; infertility;  
 KW glomerulonephritis; bullous pemphigoid; Sjogren's syndrome;  
 KW diabetes mellitus; chronic active hepatitis; primary biliary cirrhosis;  
 KW vitiligo; vasculitis; cardiotomy syndrome; urticaria; atopic dermatitis;  
 KW asthma; inflammatory myopathy; inflammatory skin disease; psoriasis;  
 KW sclerosis; inflammatory bowel disease; Crohn's disease;  
 KW ulcerative colitis; respiratory distress syndrome;  
 KW adult respiratory distress syndrome; ARDS; meningitis; encephalitis;  
 KW colitis; allergy; eczema.  
 OS Homo sapiens.  
 XX  
 PN US2004048296-A1.  
 XX  
 PD 11-MAR-2004.  
 XX  
 PF 15-JUL-2003; 2003US-00618797.  
 XX  
 PR 05-MAY-2000; 2000US-0202193P.  
 PR 04-MAY-2001; 2001US-00848295.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Baker KP, N1 J;  
 XX  
 XX WPI; 2004-226194/21.  
 DR N-PSDB; ADJ92511.  
 XX  
 PT New isolated human tumor necrosis factor TR20 polypeptide and nucleic  
 PT acid molecule, useful for diagnosing or treating conditions with aberrant  
 PT expression of the TR20 polypeptide, such as immunodeficiency and  
 PT autoimmune diseases.  
 XX  
 PS Disclosure; SEQ ID NO 2; 114pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid. The nucleic acid and  
 CC its protein are useful for the diagnosis and/or treatment of  
 CC immunodeficiency and/or autoimmune diseases or conditions associated with  
 CC aberrant expression or activity of the TR20 polypeptide, such as severe  
 CC combined immunodeficiency (SCID)-X linked, SCID-autosomal, adenosine  
 CC deaminase deficiency (ADA deficiency), X-linked agammaglobulinemia  
 CC (XLA), Bruton's disease, congenital agammaglobulinemia, X-linked  
 CC infantile agammaglobulinemia, acquired agammaglobulinemia, adult onset  
 CC agammaglobulinemia, late-onset agammaglobulinemia,  
 CC dysagammaglobulinemia, hypogammaglobulinemia, transient  
 CC hypogammaglobulinemia of infancy, unspecified hypogammaglobulinemia,  
 CC agammaglobulinemia, common variable immunodeficiency (CVID), Wiskott-  
 CC Aldrich Syndrome (WAS), X-linked immunodeficiency with hyper IgM, non X-  
 CC linked immunodeficiency (ADA deficiency), X-linked immunodeficiency with hyper IgM, non X-  
 CC linked immunodeficiency with hyper IgM, selective IGA deficiency, IGG  
 CC subclass deficiency (with or without IGA deficiency), antibody deficiency  
 CC with normal or elevated Igs, immunodeficiency with thymoma, Ig heavy  
 CC chain deletions, kappa chain deficiency, B cell lymphoproliferative  
 CC disorder (BLPD), selective IgM immunodeficiency, recessive  
 CC agammaglobulinemia (Swiss type), reticular dysgenesis, neonatal  
 CC neutropenia, severe congenital leukopenia, thymic lymphoplasia-aplasia  
 CC or dysplasia with immunodeficiency, ataxia-telangiectasia, short limbed  
 CC dwarfism, X-linked lymphoproliferative syndrome (XLP), Nezelof syndrome-

CC combined immunodeficiency with Igs, purine nucleoside phosphorylase  
 CC deficiency (PNP), MHC Class II deficiency (Bare Lymphocyte Syndrome), and  
 CC severe combined immunodeficiency. The autoimmune disease is a member  
 CC selected from the group consisting of autoimmune haemolytic anaemia  
 CC (including cryoglobulinemia or Coombs positive anaemia), autoimmune  
 CC neonatal thrombocytopenia, idiopathic thrombocytopenia purpura,  
 CC antithrombocytopenia, autoimmune neutropenia, haemolytic anaemia,  
 CC antiphospholipid syndrome, dermatitis (e.g. atopic dermatitis), allergic  
 CC encephalomyelitis, myocarditis, relapsing polychondritis, rheumatic heart  
 CC disease, glomerulonephritis (IGA nephropathy), Multiple Sclerosis,  
 CC Neuritis, Uveitis Ophthalmia, Polyendocrinopathies, Purpura (e.g. Henoch  
 CC -Schonlein purpura), Reiter's Disease, Stiff-Man Syndrome, Autoimmune  
 CC Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent  
 CC diabetes mellitus, juvenile onset diabetes, and autoimmune inflammatory  
 CC eye, autoimmune thyroiditis, hypothyroidism (i.e. Hashimoto's  
 CC thyroiditis, systemic lupus erythematosus, Goodpasture's syndrome,  
 CC Pemphigus, Receptor autoantibodies such as, Graves Disease, Myasthenia  
 CC Gravis, and insulin resistance, autoimmune thrombocytopenic purpura,  
 CC rheumatoid arthritis, gluten-sensitive enteropathy, dense deposit  
 CC disease, scleroderma with anti-collagen antibodies, mixed connective  
 CC tissue disease, polymyositis/dermatomyositis, pernicious anaemia  
 CC (Addison's disease), idiopathic Addison's disease, infertility,  
 CC Glomerulonephritis such as primary glomerulonephritis and IGA  
 CC nephropathy, bullous pemphigoid, Sjogren's syndrome, diabetes mellitus,  
 CC chronic active hepatitis, primary biliary cirrhosis, other endocrine  
 CC gland failure, vitiligo, vasculitis, post-MI, cardiomyopathy, and other  
 CC inflammatory, granulomatous, degenerative, atrophic disorders, and other  
 CC disorders such as inflammatory skin diseases including psoriasis and  
 CC sclerosis, inflammatory bowel diseases (such as Crohn's disease and  
 CC ulcerative colitis), respiratory distress syndrome (including adult  
 CC respiratory distress syndrome, ARDS), meningitis, encephalitis, colitis,  
 CC allergic conditions such as eczema and other conditions involving  
 CC infiltration of T cells and chronic inflammatory responses,  
 CC atherosclerosis, leukocyte adhesion deficiency, Reynaud's syndrome, and  
 CC immune responses associated with acute and delayed hypersensitivity  
 CC mediated by cytokines and T-lymphocytes typically found in tuberculosis,  
 CC sarcoidosis, granulomatosis and diseases involving leukocyte diapedesis,  
 CC central nervous system (CNS) inflammatory disorder, multiple organ injury  
 CC syndrome, antigen-antibody complex mediated diseases, anti-glomerular  
 CC basement membrane disease, Lambert-Eaton myasthenia syndrome, Behcet  
 CC disease, giant cell arteritis, immune complex nephritis, IGA nephropathy,  
 CC IgM polyneuropathies or autoimmune thrombocytopenia. The present sequence  
 CC represents the amino acid sequence of human IF20.

XX Sequence 142 AA;

Query Match 100.0%; Score 803; DB 8; Length 142;  
 Best Local Similarity 100.0%; Pred. No. 3e-69;  
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSCPQYWAALLGTCMFKCAICNHOSQRTCAASCGEFWDLSPGDSVITPNACPOSTLW 60  
 |||||  
 Db 1 MRSCPQYWAALLGTCMFKCAICNHOSQRTCAASCGEFWDLSPGDSVITPNACPOSTLW 60  
 |||||

QY 61 PHSQVAERAGDVCGTSPSTELLWPHCLLSVSNMPCSSLPRVLCTCCSCLCMLS 120  
 |||||  
 Db 61 PHSQVAERAGDVCGTSPSTELLWPHCLLSVSNMPCSSLPRVLCTCCSCLCMLS 120  
 |||||

QY 121 IIFPQLPPTQLSLGPNIGILL 142  
 |||||  
 Db 121 IIFPQLPPTQLSLGPNIGILL 142  
 |||||

RESULT 3  
 AAE29295  
 ID AAE29295 standard; protein; 154 AA.  
 XX AAE29295;  
 AC AAE29295;  
 DT 27-JAN-2003 (first entry)  
 XX Human gene 6 encoded protein HPMKI40, SEQ ID NO:22.

XX Human; immune system disorder; HIV infection; myocardial infarction;  
 KW human immunodeficiency virus; arthritis; hyperproliferative disease;  
 KW acquired immune deficiency syndrome; inflammation; asthma; myopathy;  
 KW allergy; cancer; cardiac oedema; duodenal ulcer; psoriasis; sepsis;  
 KW neuromuscular system disorder; multiple myeloma; pulmonary disorder;  
 KW cardiovascular disorder; rhabdomyosarcoma; gastrointestinal disorder;  
 KW multiple sclerosis; immune-mediated thrombocytopenia; myocarditis;  
 KW leiomyosarcoma; autoimmune disorder; Crohn's disease; gene therapy;  
 KW hyperaemia; AIDS; infection.  
 XX Homo sapiens.

Key Location/Qualifiers  
 Misc-difference 100 /label= Unknown  
 FT /note= "Encoded by TGG"  
 FT Misc-difference 126 /label= Unknown  
 FT /note= "Encoded by TYC"  
 FT Misc-difference 151 /label= Unknown  
 FT /note= "Encoded by YCT"  
 FT Misc-difference 153 /label= Unknown  
 FT /note= "Encoded by KAC"  
 XX WO200272763-A2.  
 XX 19-SEP-2002.  
 XX 08-MAR-2002; 2002WO-US006990.  
 XX 09-MAR-2001; 2001US-0274214P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Shi Y, Ni J, Ruben SM;  
 XX WPI; 2002-759842/82.  
 XX N-PSDB; AAD46954.  
 XX New proteins encoded by genes contained in cDNA clones (e.g. HAPQL38 or  
 XX HFO577), useful for preventing, treating, ameliorating or diagnosing  
 XX e.g. AIDS, sepsis, brain cancer, Crohn's disease or myocardial  
 XX infarction.

Claim 11; Page 420-421; 429pp; English.

XX AAD46949-AAD46954 represent cDNAs corresponding to novel human protein  
 XX genes, and AAE29290-AAE29295 represent the proteins they encode. AAD46955  
 XX -AAD46963 represent novel human protein genes and AAE29296-AAE29297  
 XX represent novel human protein fragments. Sequences of the inventions are  
 XX useful for preventing, treating or ameliorating medical conditions or for  
 XX wound healing. These conditions include diseases or disorders of the  
 XX immune system (e.g. HIV infection, autoimmune disorders, arthritis,  
 XX asthma, AIDS, sepsis, psoriasis or inflammation) or neuromuscular system  
 XX (e.g. multiple sclerosis, myocarditis, or myopathies), disorders  
 XX associated with FC receptor binding by antibody (e.g. immune-mediated  
 XX thrombocytopenia, inflammatory responses or allergic responses),  
 XX hyperproliferative diseases (e.g. multiple myeloma, rhabdomyosarcoma,  
 XX lung cancer, brain cancer or leiomyosarcoma), gastrointestinal disorders  
 XX (e.g. Crohn's disease or duodenal ulcers), pulmonary disorders, cardiac  
 XX infections or cardiovascular disorders (e.g. hyperaemia, myocardial  
 XX infarction or cardiac oedema). The invention is useful in gene therapy.  
 XX The present sequence represents human protein of the invention

XX Sequence 154 AA;

Query Match 86.9%; Score 697.5; DB 5; Length 154;  
 Best Local Similarity 92.7%; Pred. No. 4.7e-59;  
 Matches 127; Conservative 0; Mismatches 3; Indels 7; Gaps 1;



```

QY 1 MRSCPEQYWAALLGTCMFCKAICNHQSORTCAASC-----GEFWDLSFGDSVITPNA 60
D 1 MRSCPEQYWAALLGTCMFCKAICNHQSORTCAASC-----GEFWDLSFGDSVITPNA 60
QY 61 PHSQVAERWAGGVDVCGTSPSTFLWPHCLLSVSNMPCSSLPRLVLTCTCCSRCLCMLS 120
D 61 PHSQVAERWAGGVDVCGTSPSTFLWPHCLLSVSNMPCSSLPRLVLTCTCCSRCLCMLS 120
QY 121 IIFPQLPPTQLSLGPN 137
D 121 IIF-----LSXILPN 130

RESULT 4
ADZ67771
ID ADZ67771 standard; protein; 292 AA.
XX
AC ADZ67771;
XX
DT 14-JUL-2005 (first entry)
XX
DE Human tumor necrosis factor receptor TACI.
XX
KW Tumor necrosis factor receptor; TACI; cancer; neoplasm; diagnosis;
KW cytosstatic.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Domain 22..43
FT /note= "Cys-rich domain"
XX
PN WO2005037865-A2.
XX
PD 28-APR-2005.
XX
PF 18-OCT-2004; 2004WO-US034375.
XX
PR 16-OCT-2003; 2003US-0511698P.
PR 18-OCT-2004; 2004US-0619552P.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Fox BA, Holloway JL, Sheppard PO, Dillon SR;
XX
DR WPI; 2005-315682/32.
XX
PT New tumor necrosis factor receptor (TNFR) polypeptides, useful as
PT detecting ligands, and for modulating tumor growth, metastasis and
PT immunity, such as separating resting from stimulated immune cells.
XX
PS Disclosure; SEQ ID NO 19; 132pp; English.
XX
CC The invention provides novel tumor necrosis factor receptor (TNFR)
CC znfr14 polynucleotides ADZ67753 and polypeptides ADZ67754, expression
CC vectors and antibodies. Znfr14 polynucleotides are used in claimed
CC methods for detecting a genetic abnormality in a patient and for
CC detecting a cancer in a patient. Recombinant znfr14 polypeptide,
CC optionally conjugated to a toxin, is used in a claimed method of killing
CC cancer cells. Znfr14 polypeptides can be used to detect ligands,
CC agonists and antagonists. The polypeptides, polynucleotides and
CC antibodies may also be used in methods that modulate tumor growth,
CC metastasis, and immunity such as separating resting from stimulated
CC immune cells. The present sequence is that of human TNFR TACI. This
CC sequence was compared with that of znfr14 in the identification of
CC znfr14 as a member of the TNFR family.
XX
SQ Sequence 292 AA;
Query Match 24.8%; Score 199.5; DB 9; Length 292;
Best Local Similarity 27.1%; Pred. No. 7.8e-11;
Matches 62; Conservative 10; Mismatches 52; Indels 105; Gaps 6;

```

```

QY 1 MRSCPEQYWAALLGTCMFCKAICNHQSORTCAASC-----GEFWDLSFGDSVITP 51
D 31 MRSCPEQYWDPLLTGTCMSCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90
QY 52 NACPQS-----TLWPHSOVAERWAGGVDV----- 76
D 91 SICGQHPKQCAYPECNKLRSPVNLPELR-----RQSRGEVNNNSDGRYQGLEHRGSEA 146
QY 77 -----CGTSPSTFLWPHCLLSVSNMPCSSLPRLV----- 107
D 147 SPALPGLKLSADQVALVYSTGLCLCAVLCLVAVACFLKRGDPCSCQPRRQSPA 206
QY 108 -----CTCCSRCLCMLSIIFFQLPPTQLSLG 136
D 207 KSSQDHAMEAGSPVSTSPBVTCSFC-----FFCRAPTOESAVTP 247

RESULT 5
AAU10949
ID AAU10949 standard; protein; 291 AA.
XX
AC AAU10949;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human AGP-3 receptor extracellular domain.
XX
KW Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;
KW dermatological; neuroprotective; nootropic; immunomodulator; metabolic;
KW antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever;
KW antiparkinsonian; antipsoriatic; vasotropic; antibacterial; asthma;
KW AGP-3 receptor; tumor necrosis factor ligand family; AGP-3 receptor;
KW mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder;
KW rheumatoid arthritis; graft-versus-host disease; Crohn's disease;
KW pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease;
KW diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia;
KW multiple sclerosis; Parkinson's disease; transgenic animal.
XX
OS Homo sapiens.
XX
PN WO200185782-A2.
XX
PD 15-NOV-2001.
XX
PF 12-FEB-2001; 2001WO-US004568.
XX
PR 11-FEB-2000; 2000US-0181800P.
XX
PA (AMGR-) AMGEN INC.
XX
PI Boyle WJ, Hsu H;
XX
DR WPI; 2002-049441/06.
XX
PT Composition, useful for identifying modulator of receptor for treating
PT asthma and glomerulonephritis, comprises AGP-3 (tumor necrosis factor
PT ligand family member) receptor and encoding nucleic acids.
XX
PS Claim 1; Fig 18; 124pp; English.
XX
CC The invention relates to a composition (I) comprising AGP-3 receptor
CC (tumor necrosis factor ligand family member) related protein (II)
CC attached to a vehicle protein. (I) is useful for modulating AGP-3-related
CC activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in
CC assays to identify cells and tissues that express AGP-3R or proteins
CC related to AGP-3R-related protein and for identifying compounds (agonists
CC or antagonists) that interact with AGP-3R proteins. (II) is also useful
CC for identifying intracellular proteins that interact with the respective
CC cytoplasmic domains by yeast two-hybrid screening process. (II) is
CC involved in B cell growth, survival and activation particularly in lymph
CC node, spleen, and Peyer's patches. AGP-3R agonists and antagonists
CC identified using (II) are used for modulating B cell response and are
CC used to treat diseases characterised by inflammatory processes or

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deregulated immune response such as rheumatoid arthritis, graft-versus-host disease, Crohn's disease, lupus, etc. (II) is also useful in the production of hybridoma cells which are derived from B cells, which involves treating the hybridoma cells with (II). (II) is useful in the treatment of inflammatory conditions of joints, e.g., rheumatoid arthritis, osteoarthritis, etc. (II), its agonists or antagonists are useful for treating acute pancreatitis, amyotrophic lateral sclerosis (ALS), Alzheimer's disease, asthma, atherosclerosis, cachexia/anorexia, diabetes, fever, glomerulonephritis, inflammatory bowel disease, ischaemic injury including cerebral ischaemia, multiple myeloma, multiple sclerosis, osteoporosis, Parkinson's disease, pain, reperfusion injury, septic shock, etc. The nucleic acids are also useful for developing transgenic animals expressing (II), which are useful for producing the polypeptides and for the study of in vivo biological activity. The present sequence represents the amino acid sequence of human AGP-3 extracellular domain

XX SQ Sequence 291 AA;

Query Match 24.7%; Score 198.5; DB 5; Length 291;  
Best Local Similarity 27.1%; Pred. No. 9.7e-11;  
Matches 62; Conservative 12; Mismatches 50; Indels 105; Gaps 7;

QY 1 MRSCEQYWAALLGTCMFCCKAICNHQSORTCAASC-----GEFWDLSQDSVITP 51  
DB 31 MRSCEQYWDPLGTCMCKTICNHQSORTCAAFCSRSLCRKEQKGFYDHLRLDCISCA 90  
QY 52 NACPQS-----TLPHSQVAERMGAGDVQ----- 76  
DB 91 SICGQHPKQCAVFCENKLRSPVNLPELR----RQRSGEVNNSDNGRYQGLEHGRSEA 146  
QY 77 -----CGTSYPSFTLLWPHCLLSVSNMPCSSLPRVL----- 107  
DB 147 SPALPGLKLSADQVAVYSTGLCLCAVLCCFLVAVACFLKMGDPCSCQPRSPROSPA 206  
QY 108 -----CTCCSRCLCMLSIIFPOL-PPTQLSGLGP 136  
DB 207 SSQDHAMEAGSPVSTSPVETCSFC-----FPCECRPTQESAVTP 247

RESULT 6

AAU09900  
ID AAU09900 standard; protein; 293 AA.

AC AAU09900;

DT 12-MAR-2002 (first entry)

DE Human AGP-3 related protein receptor.

XX Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;  
KW dermatological; neuroprotective; nontropic; immunomodulator; metabolic;  
KW antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever;  
KW antiparkinsonian; antipsoriatic; vasotropic; antibacterial; asthma;  
KW AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor;  
KW mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder;  
KW rheumatoid arthritis; graft-versus-host disease; Crohn's disease;  
KW pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease;  
KW diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia;  
KW multiple sclerosis; Parkinson's disease; transgenic animal.

OS Homo sapiens.

XX WO200185782-A2.

PN 15-NOV-2001.

XX 12-FEB-2001; 2001WO-US0004568.

XX 11-FEB-2000; 2000US-0181800P.

XX (AMGE-) AMGEN INC.

PI Boyle WJ, Hsu H;  
XX WPI; 2002-049441/06.  
DR N-PSDB; AAS18558.  
XX

Composition, useful for identifying modulator of receptor for treating asthma and glomerulonephritis, comprises AGP-3 (tumour necrosis factor ligand family member) receptor and encoding nucleic acids.

XX Disclosure; Page 117-119; 124pp; English.

XX The invention relates to a composition (I) comprising AGP-3 receptor (tumour necrosis factor ligand family member) related protein (II) attached to a vehicle protein. (I) is useful for modulating AGP-3-related activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in assays to identify cells and tissues that express AGP-3R or proteins related to AGP-3R-related protein and for identifying compounds (agonists or antagonists) that interact with AGP-3R proteins. (II) is also useful for identifying intracellular proteins that interact with the respective cytoplasmic domains by yeast two-hybrid screening process. (II) is involved in B cell growth, survival and activation particularly in lymph node, spleen, and Peyer's patches. AGP-3R agonists and antagonists identified using (II) are used for modulating B cell response and are used to treat diseases characterised by inflammatory processes or deregulated immune response such as rheumatoid arthritis, graft-versus-host disease, Crohn's disease, lupus, etc. (II) is also useful in the production of hybridoma cells which are derived from B cells, which involves treating the hybridoma cells with (II). (II) is useful in the treatment of inflammatory conditions of joints, e.g., rheumatoid arthritis, osteoarthritis, etc. (II), its agonists or antagonists are useful for treating acute pancreatitis, amyotrophic lateral sclerosis (ALS), Alzheimer's disease, asthma, atherosclerosis, cachexia/anorexia, diabetes, fever, glomerulonephritis, inflammatory bowel disease, ischaemic injury including cerebral ischaemia, multiple myeloma, multiple sclerosis, osteoporosis, Parkinson's disease, pain, reperfusion injury, septic shock, etc. The nucleic acids are also useful for developing transgenic animals expressing (II), which are useful for producing the polypeptides and for the study of in vivo biological activity. The present sequence represents the amino acid sequence of human AGP-3 related protein receptor

XX SQ Sequence 293 AA;

Query Match 24.7%; Score 198; DB 5; Length 293;  
Best Local Similarity 27.0%; Pred. No. 1.1e-10;  
Matches 62; Conservative 12; Mismatches 50; Indels 106; Gaps 7;

QY 1 MRSCEQYWAALLGTCMFCCKAICNHQSORTCAASC-----GEFWDLSQDSVITP 51  
DB 31 MRSCEQYWDPLGTCMCKTICNHQSORTCAAFCSRSLCRKEQKGFYDHLRLDCISCA 90  
QY 52 NACPQS-----TLPHSQVAERMGAGDVQ----- 76  
DB 91 SICGQHPKQCAVFCENKLRSPVNLPELR----RQRSGEVNNSDNGRYQGLEHGRSEA 146  
QY 77 -----CGTSYPSFTLLWPHCLLSVSNMPCSSLPRVL----- 107  
DB 147 SPALPGLKLSADQVAVYSTGLCLCAVLCCFLVAVACFLKMGDPCSCQPRSPROSPA 206  
QY 108 -----CTCCSRCLCMLSIIFPOL-PPTQLSGLGP 136  
DB 207 KSSQDHAMEAGSPVSTSPVETCSFC-----FPCECRPTQESAVTP 248

RESULT 7

AAE09244

ID AAE09244 standard; protein; 265 AA.

XX AAE09244;

DT 19-NOV-2001 (first entry)

XX Human TACI splice variant protein.

XX Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;  
 KW TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;  
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.  
 XX Homo sapiens.  
 OS  
 PN WO200160397-A1.  
 XX  
 PD 23-AUG-2001.  
 XX  
 PF 28-NOV-2000; 2000WO-US032378.  
 XX  
 PR 16-FEB-2000; 2000US-0182938P.  
 XX  
 PR 22-AUG-2000; 2000US-0226986P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;  
 PI Yan M;  
 XX  
 DR WPI; 2001-541628/60.  
 XX  
 XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological  
 PT activity, for treating autoimmune disorders and cancer, comprises  
 PT exposing the cells to TALL-1 or APRIL polypeptide agonists or  
 PT antagonists.  
 XX  
 PS Example 1; Fig 6; 160pp; English.  
 XX  
 CC The invention relates to methods of using one or more agonists or  
 CC antagonists to modulate the activity of the members of TNF (tumour  
 CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.  
 CC TACI or BCMA. The method is useful for treating pathological conditions  
 CC or diseases associated with increased TALL-1 and APRIL expression or  
 CC activity. TALL-1 and APRIL antagonists are used to block the interaction  
 CC between APRIL and TALL-1 with TACI or BCMA. They are useful for treating  
 CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,  
 CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid  
 CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The  
 CC present sequence is human TACI splice variant protein  
 XX  
 SQ Sequence 265 AA;  
 Query Match 24.3%; Score 195; DB 4; Length 265;  
 Best Local Similarity 27.0%; Pred. No. 1.9e-10;  
 Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;  
 QY 1 MRSCPEQYWAALLGTCMFCCKAICNHQSORTCAASC-----GEFWDLSFGDSVITP 51  
 DB 31 MRSCPEQYWDPLGTGCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90  
 QY 52 NACPQS-----TLWPHSQAVERMAGDVQ----- 76  
 DB 91 SICGQHPKQCAFCENKLRSPVNLPELR-----RQRSGEVENNSDNGRYQGLEHRGSEA 146  
 QY 77 -----CGTSYPSFTLLWPHCLLSVSNMPCSSLPRVL----- 107  
 DB 147 SPALPGLKLSADQVALVYSTGLGLCAVLCCFLVAVACFLKKGDFCSCQPRSRPRQSPA 206  
 QY 108 -----CTCCSRCLCMLSIIFPOL-PPQLSLGLP 136  
 DB 207 KSSQDHAMEAGSPVSTSPVPVETCSFC-----PFECRAPTQESAVTP 248  
 QY 77 -----CGTSYPSFTLLWPHCLLSVSNMPCSSLPRVL----- 107  
 DB 147 SPALPGLKLSADQVALVYSTGLGLCAVLCCFLVAVACFLKKGDFCSCQPRSRPRQSPA 206  
 QY 108 -----CTCCSRCLCMLSIIFPOL-PPQLSLGLP 136  
 DB 207 KSSQDHAMEAGSPVSTSPVPVETCSFC-----PFECRAPTQESAVTP 248  
 RESULT 8  
 ABP97723  
 ID ABP97723 standard; protein; 266 AA.  
 XX  
 AC ABP97723;  
 XX  
 XX 28-MAY-2003 (first entry)  
 DT  
 XX

DE Amino acid sequence of an alternatively spliced human TACI receptor.  
 XX Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;  
 KW TALL-1; April; systemic lupus erythematosus.  
 XX Homo sapiens.  
 OS  
 PN WO2003014294-A2.  
 XX  
 PD 20-FEB-2003.  
 XX  
 PF 24-JUL-2002; 2002WO-US023487.  
 XX  
 PR 03-AUG-2001; 2001US-0310114P.  
 XX  
 PR 30-APR-2002; 2002US-0377171P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 XX Dixit V, Grewal I, Ridgway J, Yan M;  
 PI WPI; 2003-256560/25.  
 XX  
 DR WPI; 2003-256560/25.  
 XX  
 XX New nucleic acid encoding a TACIs or BR3 polypeptide, useful for  
 PT preparing a composition for treating systemic lupus erythematosus.  
 XX  
 PS Disclosure; Fig 8; 153pp; English.  
 XX  
 CC The present sequence represents an alternatively spliced human TACI  
 CC polypeptide. The specification also describes BR3 polypeptides. TACI and  
 CC BR3 are receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and  
 CC April bind to the TACI receptor, while TNF family ligands TALL-1 also  
 CC binds to BR3 receptor. The TACI and BR3 receptor nucleic acid is useful  
 CC for preparing a composition for treating systemic lupus erythematosus  
 XX  
 SQ Sequence 266 AA;  
 Query Match 24.3%; Score 195; DB 6; Length 266;  
 Best Local Similarity 27.0%; Pred. No. 1.9e-10;  
 Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;  
 QY 1 MRSCPEQYWAALLGTCMFCCKAICNHQSORTCAASC-----GEFWDLSFGDSVITP 51  
 DB 31 MRSCPEQYWDPLGTGCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90  
 QY 52 NACPQS-----TLWPHSQAVERMAGDVQ----- 76  
 DB 91 SICGQHPKQCAFCENKLRSPVNLPELR-----RQRSGEVENNSDNGRYQGLEHRGSEA 146  
 QY 77 -----CGTSYPSFTLLWPHCLLSVSNMPCSSLPRVL----- 107  
 DB 147 SPALPGLKLSADQVALVYSTGLGLCAVLCCFLVAVACFLKKGDFCSCQPRSRPRQSPA 206  
 QY 108 -----CTCCSRCLCMLSIIFPOL-PPQLSLGLP 136  
 DB 207 KSSQDHAMEAGSPVSTSPVPVETCSFC-----PFECRAPTQESAVTP 248  
 RESULT 9  
 ADW03442  
 ID ADW03442 standard; protein; 266 AA.  
 XX  
 AC ADW03442;  
 XX  
 XX 24-MAR-2005 (first entry)  
 DT  
 XX  
 DE Human TACI protein amino acid sequence #3.  
 XX  
 KW B-lymphocyte; b-cell lymphoma; autoimmune disease; immunosuppressive;  
 KW non-hodgkin lymphoma; hodgkins disease; cytostatic;  
 KW chronic lymphocytic leukemia; hairy cell leukemia; rheumatoid arthritis;  
 KW antiarthritic; antirheumatic; systemic lupus erythematosus;  
 KW wegner granulomatosis; antiallergic; antiinflammatory; vasotropic;  
 KW inflammatory bowel disease; gastrointestinal-gen.;





CC receptor-ligand engagement is associated with asthma, bronchitis,  
CC emphysema, end stage renal failure, glomerulonephritis, vasculitis,  
CC nephritis, pyelonephritis, renal neoplasms, multiple myelomas, lymphomas,  
CC light chain neuropathy, amyloidosis, moderating immune response,  
CC immunosuppression, graft rejection, graft versus host disease,  
CC inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint  
CC pain, swelling, anaemia, or septic shock, BR43x2, TACI and BCMA  
CC polypeptides, fusions, antibodies, agonists or antagonists can be used to  
CC treat hypertension, renal artery stenosis, or occlusion, and cholesterol  
CC or renal emboli  
XX  
SQ Sequence 293 AA;

**SQ Sequence 293 AA;**

```

Query Match      24.3%; Score 195; DB 3; Length 293;
Best Local Similarity 27.0%; Pred. No. 2.1e-10;
Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

QY      1 MRSCEPQYWAALIGTCMFKCAI CNHQSORTCAASC-----GEFDLSPGDSVITP 51.
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      31 MRSCEPQYWDPLIGTCMSCKTICNHQSORTCAAFCSLSCKRGQKPYDHLRDCISCA 90
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      52 NACEQS-----TLWPHSQVAEERVAGGDVQ-----76
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Db      91 SICQHPKQCA YFCENKLRSPVNLPELR-----RQRSEVENNSDNGRYQGLEHRGSEA 146
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      77 -----CGTSVPSTFLWPHCLLSVSNMPCSSLSRVL-----107
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db      147 SPALPGLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKRGDPCSCQPSRPRQSPA 206
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      108 -----CTCCGRCLCEMLSIIFPOL--PPTQLSGLGP 136
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db      207 KSSQDHAMEAGSPVSTSPVETCSFC-----PPECRAFTQESAVTP 248
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

## RESULT 13

AAE09240  
ID AAE09240 standard; protein; 293 AA.

AC AAE09240:

19-NOV-2001 (first entry)

Human TACT protein.

Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma; autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.

XX PN W0200160397-A1

XX PD 23-AUG-2001.

XX  
DD  
28-NOV-2000.

16-888-3000 • 3000US-0183828P  
XX BB

PR 22-AUG-2000; 2000US-0226986P.  
yy

PA (GETH ) GENENTECH INC.

PI Ashkenazi AJ, Dodge K

XX

DR N-PSDB; AAD15901.

PT Inhibiting or neu

PT exposing the cells to TALL-1 or APRIL polypeptide agonists or PT antagonists.

Example 1: Fig 1; 160pp; English.

XX CC The invention relates to methods of using one or more agonists or  
CC antagonists to modulate the activity of the members of TNF (tumour  
CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.  
CC TACI or BCMA. The method is useful for treating pathological conditions  
CC or diseases associated with increased TALL-1 and APRIL expression or  
CC activity. TALL-1 and APRIL antagonists are used to block the interaction  
CC between APRIL and TALL-1 with TACI or BCMA. They are useful for treating  
CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,  
CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid  
CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The  
CC present sequence is human TACI protein

Sequence 293 AA:

[illegible]

RESUM.T 14

AA71914

XX  
ID  
AAI/1914

AC  
XX  
AAV/1914;

DT 26-MAR-2001 (first entry)  
YY

DE Human tumour necrosis factor receptor (TACI) protein.  
XX  
XX Human; transmembrane activator and CAML interactor; TACI;  
KW tumour necrosis factor receptor; TNF; autoimmune disease;  
KW calcium-signal modulating cyclophilin ligand; CAML; viral infection;  
KW neutrokin alpha polypeptide; TACI-Ligand; TACI-L; cytostatic; therapy;  
KW neuroprotective; anti-diabetic; antiviral; anti-inflammatory; tumour;  
KW antiarthritic; anti-rheumatic; immunosuppressive; multiple sclerosis;  
KW rheumatoid arthritis; Graft rejection; inflammation; cell proliferation;  
KW cell death; immunoglobulin E-mediated allergic reaction; IGE.  
XX

OS Homo sapiens.

XX	Key	Location/Qualifiers
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4	4	4
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92	92	92
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97	97	97
98	98	98
99	99	99
100	100	100

ET  
ET  
DOLLAR

FT  
domain of TACT-I." /note= "Binds with amino acids 123-285 of extracellular

XX, W0200057034-A1

XX 25 MAY 2000

1000

XX

XX

XX



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OM protein - protein search, using sw model

Run on: December 20, 2005, 10:33:33 ; Search time 65 Seconds  
(without alignments)

912.796 Million cell updates/sec

Title: US-10-618-797-2

Perfect score: 803

Sequence: 1 MRSCPEQYWAALLGTCMFC.....FPQLPPTQLSLGPNIGLL 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA\_Main:\*

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3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*

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6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	198.5	24.7	291	3	US-09-779-050A-43
3	198	24.7	293	3	US-09-779-050A-42
4	195	24.3	265	5	US-10-626-914-17
5	195	24.3	265	5	US-10-485-489-19
6	195	24.3	265	5	US-10-861-049-36
7	195	24.3	265	6	US-11-021-874-36
8	195	24.3	293	3	US-09-879-919-22
9	195	24.3	293	3	US-09-854-864-14
10	195	24.3	293	3	US-09-855-158-14
11	195	24.3	293	3	US-09-961-376-2
12	195	24.3	293	3	US-09-302-863-2
13	195	24.3	293	3	US-09-855-564-2
14	195	24.3	293	4	US-10-087-192-1650
15	195	24.3	293	4	US-10-084-971-2
16	195	24.3	293	4	US-10-068-725-4
17	195	24.3	293	4	US-10-151-882-46
18	195	24.3	293	4	US-10-233-816-2
19	195	24.3	293	4	US-10-008-063-8
20	195	24.3	293	4	US-10-152-363A-2
21	195	24.3	293	4	US-10-268-951-22
22	195	24.3	293	4	US-10-258-368-1
23	195	24.3	293	4	US-10-618-797-4
24	195	24.3	293	4	US-10-742-634-7
25	195	24.3	293	4	US-10-748-112-27
26	195	24.3	293	5	US-10-684-149-4
27	195	24.3	293	5	US-10-626-914-3

28 195 24.3 293 5 US-10-485-489-3 Sequence 3, Appli

29 195 24.3 293 5 US-10-861-049-25 Sequence 25, Appli

30 195 24.3 293 6 US-11-021-874-25 Sequence 25, Appli

31 195 24.3 293 6 US-11-079-418-2 Sequence 2, Appli

32 195 24.3 301 4 US-10-258-368-12 Sequence 12, Appli

33 193 24.0 344 4 US-10-152-363A-52 Sequence 52, Appli

34 192.5 24.0 166 3 US-09-854-864-15 Sequence 15, Appli

35 192.5 24.0 166 3 US-09-855-158-15 Sequence 15, Appli

36 192.5 24.0 166 4 US-10-293-816-6 Sequence 6, Appli

37 192.5 24.0 171 5 US-11-079-418-6 Sequence 6, Appli

38 192.5 24.0 332 4 US-10-684-149-18 Sequence 18, Appli

39 192.5 24.0 332 4 US-10-152-363A-62 Sequence 62, Appli

40 192.5 24.0 348 4 US-10-152-363A-54 Sequence 54, Appli

41 192.5 24.0 357 4 US-10-152-363A-56 Sequence 56, Appli

42 192.5 24.0 366 4 US-10-258-368-6 Sequence 6, Appli

43 192.5 24.0 392 4 US-10-152-363A-50 Sequence 50, Appli

44 192.5 24.0 397 3 US-09-854-864-18 Sequence 18, Appli

45 192.5 24.0 397 3 US-09-855-158-18 Sequence 18, Appli

#### ALIGNMENTS

##### RESULT 1

US-10-618-797-2  
; Sequence 2, Application US/10618797  
; Publication No. US20040048296A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based Thereon  
; FILE REFERENCE: PF527D1  
; CURRENT APPLICATION NUMBER: US/10/618,797  
; CURRENT FILING DATE: 2003-07-15  
; PRIOR APPLICATION NUMBER: 09/848, 295  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: 60/202,193  
; PRIOR FILING DATE: 2000-05-05  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 2  
; LENGTH: 142  
; TYPE: PRT  
; ORGANISM: human  
US-10-618-797-2

Query Match 100.0%; Score 803; DB 4; Length 142;  
Best Local Similarity 100.0%; Pred. No. 2.9e-69;  
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSCPEQYWAALLGTCMFCACNHSQRTCAASCGEFWDLSFGDSVITPNACPQSTLW 60  
Db 1 MRSCPEQYWAALLGTCMFCACNHSQRTCAASCGEFWDLSFGDSVITPNACPQSTLW 60

QY 61 PHSQVAERAGMAGDVCGTSTPSTFLWPHCLLSVSNMPCSSLPRLVCTCCSRCLCWLS 120  
Db 61 PHSQVAERAGMAGDVCGTSTPSTFLWPHCLLSVSNMPCSSLPRLVCTCCSRCLCWLS 120

QY 121 IIFPQLPPTQLSLGPNIGLL 142  
Db 121 IIFPQLPPTQLSLGPNIGLL 142

##### RESULT 2

US-09-779-050A-43  
; Sequence 43, Application US/09779050A  
; Patent No. US20020160416A1  
; GENERAL INFORMATION:  
; APPLICANT: BOYLE, WILLIAM  
; APPLICANT: HSU, HAILING  
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY  
; FILE REFERENCE: A-570B  
; CURRENT APPLICATION NUMBER: US/09/779,050A



```

; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-43

Query Match      24.7%; Score 198.5; DB 3; Length 291;
Best Local Similarity 27.0%; Pred. No. 7.9e-11;
Matches 62; Conservative 12; Mismatches 50; Indels 105; Gaps 7;

QY      1 MRSCPEQYWAALGTCMFCCKAICNHQSORTCAASC-----GEFWDLSFGDSVITP 51
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      31 MRSCPEQYWDPLGTGCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      52 NACPOS-----TLWPHSQVAERMAAGDVQ-----76
      :|||:
DB      91 SICGQHPKQCAFCENKLRSPVNLPELR-----RQRSGEVENNDSNGRYQGLEHRGSEA 146
      :|||:
QY      77 -----CGTSYPSTFLWPHCLLSVSNMPCSSLPRLV-----107
      :|||:
DB      147 SPALPGLKLSADQVAVYSTLGLCLCAVLCFLVAVACFLKMRGDPSCQPSRSPRQSPAK 206
      :|||:
QY      108 -----CTCCSRCLCMLSIIFPOL-PPTQLSLGLP 136
      :|||:
DB      207 SSQDHAMEAGSPVSTSPFVETCSFC-----FPFCRAPTQESAVTP 247
      :|||:

RESULT 3
US-09-779-050A-42
; Sequence 42, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779, 050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-42

Query Match      24.7%; Score 198; DB 3; Length 293;
Best Local Similarity 27.0%; Pred. No. 8.8e-11;
Matches 62; Conservative 12; Mismatches 50; Indels 106; Gaps 7;

QY      1 MRSCPEQYWAALGTCMFCCKAICNHQSORTCAASC-----GEFWDLSFGDSVITP 51
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      31 MRSCPEQYWDPLGTGCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      52 NACPOS-----TLWPHSQVAERMAAGDVQ-----76
      :|||:
DB      91 SICGQHPKQCAFCENKLRSPVNLPELR-----RQRSGEVENNDSNGRYQGLEHRGSEA 146
      :|||:
QY      77 -----CGTSYPSTFLWPHCLLSVSNMPCSSLPRLV-----107
      :|||:
DB      147 SPALPGLKLSADQVAVYSTLGLCLCAVLCFLVAVACFLKMRGDPSCQPSRSPRQSPAK 206
      :|||:
QY      108 -----CTCCSRCLCMLSIIFPOL-PPTQLSLGLP 136
      :|||:
DB      207 KSSQDHAMEAGSPVSTSPFVETCSFC-----FPFCRAPTQESAVTP 248
      :|||:

; Query Match      24.3%; Score 195; DB 5; Length 265;
; Best Local Similarity 27.0%; Pred. No. 1.5e-10;
; Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

RESULT 4
US-10-626-914-17
; Sequence 17, Application US/10626914
; Publication No. US20050043516A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: CHUNTHARAPAI, ANAN
; APPLICANT: GREWAL, IQBAL
; APPLICANT: KIM, KYUNG JIN
; APPLICANT: VAN, MINHONG
; TITLE OF INVENTION: TACI Antibodies and Uses Thereof
; FILE REFERENCE: P1942R1
; CURRENT APPLICATION NUMBER: US/10/626,914
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/398,530
; PRIOR FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 17
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-626-914-17

Query Match      24.3%; Score 195; DB 5; Length 265;
Best Local Similarity 27.0%; Pred. No. 1.5e-10;
Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

QY      1 MRSCPEQYWAALGTCMFCCKAICNHQSORTCAASC-----GEFWDLSFGDSVITP 51
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      31 MRSCPEQYWDPLGTGCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      52 NACPOS-----TLWPHSQVAERMAAGDVQ-----76
      :|||:
DB      91 SICGQHPKQCAFCENKLRSPVNLPELR-----RQRSGEVENNDSNGRYQGLEHRGSEA 146
      :|||:
QY      77 -----CGTSYPSTFLWPHCLLSVSNMPCSSLPRLV-----107
      :|||:
DB      147 SPALPGLKLSADQVAVYSTLGLCLCAVLCFLVAVACFLKMRGDPSCQPSRSPRQSPAK 206
      :|||:
QY      108 -----CTCCSRCLCMLSIIFPOL-PPTQLSLGLP 136
      :|||:
DB      207 KSSQDHAMEAGSPVSTSPFVETCSFC-----FPFCRAPTQESAVTP 248
      :|||:

; Query Match      24.3%; Score 195; DB 5; Length 265;
; Best Local Similarity 27.0%; Pred. No. 1.5e-10;
; Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

RESULT 5
US-10-485-489-19
; Sequence 19, Application US/10485489
; Publication No. US20050070699A1
; GENERAL INFORMATION:
; APPLICANT: Dixit, Vishva
; APPLICANT: Grewal, Iqbal
; APPLICANT: Ridgway, John
; APPLICANT: Van, Minhong
; TITLE OF INVENTION: TACIS and BR3 Polypeptides and Uses Thereof
; FILE REFERENCE: 11669.175USWO
; CURRENT APPLICATION NUMBER: US/10/485,489
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: PCT/US02/23487
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US 60/310,114
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/377,171
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 19
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-489-19

; Query Match      24.3%; Score 195; DB 5; Length 265;
; Best Local Similarity 27.0%; Pred. No. 1.5e-10;
; Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

US-10-618-797-2rapbm
```



Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;  
Qy 1 MRSCPEQYWAALIGTCMFCKAICNHOSQRTCAASC-----GFWDLSPGDSVITP 51  
Db 31 MRSCPEQYWDPLIGTCMCKTICNHOSQRTCAAFCSRSLCRKEQKGYDHLRDCISCA 90  
Qy 52 NACPQS-----TLWPHSQVAERMAAGDVQ----- 76  
Db 91 SICQHPKQCAFCENKLRSPVNLPPELR-----RQRSEVENNSDNGRYQGLEHGRSEA 146  
Qy 77 -----CGTSPSTFLLWPHCLLSVSNMPCSSLPRLV----- 107  
Db 147 SPALPGLKLSADQVALVYSTLGLCLCAVLCFLVAVACFLKRGDPCSCQPRSRPROSPA 206  
Qy 108 -----CTCCSRCLCMLSIIFPOL-PPTQLSLGLP 136  
Db 207 KSSQDHAMEAGSPVSTSPVPVETCSFC-----PFECRAPTOESAVTP 248

RESULT 6  
US-10-861-049-36  
; Sequence 36, Application US/10861049  
; Publication No. US20050095243A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrew Chan  
; APPLICANT: Qian Gong  
; APPLICANT: Flavius Martin  
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS  
; FILE REFERENCE: P2040RIUS  
; CURRENT APPLICATION NUMBER: US/10/861,049  
; CURRENT FILING DATE: 2004-06-04  
; PRIOR APPLICATION NUMBER: US 60/476,531  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: US 60/476,481  
; PRIOR FILING DATE: 2003-06-05  
; PRIOR APPLICATION NUMBER: US 60/476,414  
; PRIOR FILING DATE: 2003-06-05  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 36  
; LENGTH: 265  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-861-049-36

Query Match 24.3%; Score 195; DB 5; Length 265;  
Best Local Similarity 27.0%; Pred. No. 1.5e-10;  
Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;  
Qy 1 MRSCPEQYWAALIGTCMFCKAICNHOSQRTCAASC-----GFWDLSPGDSVITP 51  
Db 31 MRSCPEQYWDPLIGTCMCKTICNHOSQRTCAAFCSRSLCRKEQKGYDHLRDCISCA 90  
Qy 52 NACPQS-----TLWPHSQVAERMAAGDVQ----- 76  
Db 91 SICQHPKQCAFCENKLRSPVNLPPELR-----RQRSEVENNSDNGRYQGLEHGRSEA 146  
Qy 77 -----CGTSPSTFLLWPHCLLSVSNMPCSSLPRLV----- 107  
Db 147 SPALPGLKLSADQVALVYSTLGLCLCAVLCFLVAVACFLKRGDPCSCQPRSRPROSPA 206  
Qy 108 -----CTCCSRCLCMLSIIFPOL-PPTQLSLGLP 136  
Db 207 KSSQDHAMEAGSPVSTSPVPVETCSFC-----PFECRAPTOESAVTP 248

RESULT 7  
US-11-021-874-36  
; Sequence 36, Application US/11021874  
; Publication No. US20050163775A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrew Chan  
; APPLICANT: Qian Gong  
; APPLICANT: Flavius Martin

; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS  
; FILE REFERENCE: P2040RIUS  
; CURRENT APPLICATION NUMBER: US/11/021,874  
; CURRENT FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: US 10/861,049  
; PRIOR FILING DATE: 2004-06-04  
; PRIOR APPLICATION NUMBER: US 60/476,531  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: US 60/476,481  
; PRIOR FILING DATE: 2003-06-05  
; PRIOR APPLICATION NUMBER: US 60/476,414  
; PRIOR FILING DATE: 2003-06-05  
; NUMBER OF SEQ ID NOS: 165  
; SEQ ID NO 36  
; LENGTH: 265  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-021-874-36

Query Match 24.3%; Score 195; DB 6; Length 265;  
Best Local Similarity 27.0%; Pred. No. 1.5e-10;  
Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;  
Qy 1 MRSCPEQYWAALIGTCMFCKAICNHOSQRTCAASC-----GFWDLSPGDSVITP 51  
Db 31 MRSCPEQYWDPLIGTCMCKTICNHOSQRTCAAFCSRSLCRKEQKGYDHLRDCISCA 90  
Qy 52 NACPQS-----TLWPHSQVAERMAAGDVQ----- 76  
Db 91 SICQHPKQCAFCENKLRSPVNLPPELR-----RQRSEVENNSDNGRYQGLEHGRSEA 146  
Qy 77 -----CGTSPSTFLLWPHCLLSVSNMPCSSLPRLV----- 107  
Db 147 SPALPGLKLSADQVALVYSTLGLCLCAVLCFLVAVACFLKRGDPCSCQPRSRPROSPA 206  
Qy 108 -----CTCCSRCLCMLSIIFPOL-PPTQLSLGLP 136  
Db 207 KSSQDHAMEAGSPVSTSPVPVETCSFC-----PFECRAPTOESAVTP 248

RESULT 8  
US-09-879-919-22  
; Sequence 22, Application US/09879919  
; Patent No. US20020064829A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu Guo-Liang, et al.  
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon  
; FILE REFERENCE: PF253PI  
; CURRENT APPLICATION NUMBER: US/09/879,919  
; CURRENT FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,978  
; PRIOR FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/254,875  
; PRIOR FILING DATE: 2000-12-13  
; PRIOR APPLICATION NUMBER: 60/241,952  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/211,537  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 08/815,783  
; PRIOR FILING DATE: 1997-03-12  
; PRIOR APPLICATION NUMBER: 60/016,812  
; PRIOR FILING DATE: 1996-03-14  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-879-919-22

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Query Match      24.3%; Score 195; DB 3; Length 293;
Best Local Similarity 27.0%; Pred. No. 1.7e-10;
Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

QY 1 MRSCPEEQYWAALLGTCMFCCKAICNHQSORTCAASC-----GEFWDLSPGDSVITP 51
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 31 MRSCPEEQYWDPLLGTCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 52 NACPOS-----TLWPHSQVAEREMAGGDVQ----- 76
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 91 SICGQHPKQCAFCENKLRSPVNLPPELR-----RQRSGEVNNSDNGRYQGLEHRGSEA 146
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 77 -----CGTSYPSTFLLWPHCLLSVSNMPCSSLPRVYL----- 107
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 147 SPALPGLKLSADQVALVYSTGLCLCAVLCCFLVAVACFLKKRGDFCSCQPRSRPRQSPA 206
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 108 -----CTCCSRCLCMLSIIPQL-PPTQLSLGLP 136
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 207 KSSQDHAMEAGSPVSTSPBPVETCSFC-----PFECRAPTQESAVTP 248
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
US-09-854-864-14
; Sequence 14, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-05-12
; PRIOR FILING DATE: 2000-05-12
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-14

Query Match      24.3%; Score 195; DB 3; Length 293;
Best Local Similarity 27.0%; Pred. No. 1.7e-10;
Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

QY 1 MRSCPEEQYWAALLGTCMFCCKAICNHQSORTCAASC-----GEFWDLSPGDSVITP 51
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 31 MRSCPEEQYWDPLLGTCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 52 NACPOS-----TLWPHSQVAEREMAGGDVQ----- 76
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 91 SICGQHPKQCAFCENKLRSPVNLPPELR-----RQRSGEVNNSDNGRYQGLEHRGSEA 146
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 77 -----CGTSYPSTFLLWPHCLLSVSNMPCSSLPRVYL----- 107
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 147 SPALPGLKLSADQVALVYSTGLCLCAVLCCFLVAVACFLKKRGDFCSCQPRSRPRQSPA 206
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 108 -----CTCCSRCLCMLSIIPQL-PPTQLSLGLP 136
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 207 KSSQDHAMEAGSPVSTSPBPVETCSFC-----PFECRAPTQESAVTP 248
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
US-09-855-158-14
; Sequence 14, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
```

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; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BLY
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-06-27
; PRIOR FILING DATE: 2000-06-27
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-14

Query Match      24.3%; Score 195; DB 3; Length 293;
Best Local Similarity 27.0%; Pred. No. 1.7e-10;
Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

QY 1 MRSCPEEQYWAALLGTCMFCCKAICNHQSORTCAASC-----GEFWDLSPGDSVITP 51
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 31 MRSCPEEQYWDPLLGTCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 52 NACPOS-----TLWPHSQVAEREMAGGDVQ----- 76
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 91 SICGQHPKQCAFCENKLRSPVNLPPELR-----RQRSGEVNNSDNGRYQGLEHRGSEA 146
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 77 -----CGTSYPSTFLLWPHCLLSVSNMPCSSLPRVYL----- 107
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 147 SPALPGLKLSADQVALVYSTGLCLCAVLCCFLVAVACFLKKRGDFCSCQPRSRPRQSPA 206
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 108 -----CTCCSRCLCMLSIIPQL-PPTQLSLGLP 136
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 207 KSSQDHAMEAGSPVSTSPBPVETCSFC-----PFECRAPTQESAVTP 248
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
US-09-961-376-2
; Sequence 2, Application US/09961376
; Patent No. US2002010673GAI
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR17
; FILE REFERENCE: PF524P1
; CURRENT APPLICATION NUMBER: US/09/961,376
; CURRENT FILING DATE: 2001-09-25
; PRIOR FILING DATE: 2000-12-13
; PRIOR FILING DATE: 2000-12-13
; PRIOR FILING DATE: 2000-09-26
; PRIOR FILING DATE: 2000-03-24
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-376-2

Query Match      24.3%; Score 195; DB 3; Length 293;
Best Local Similarity 27.0%; Pred. No. 1.7e-10;
Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

QY 1 MRSCPEEQYWAALLGTCMFCCKAICNHQSORTCAASC-----GEFWDLSPGDSVITP 51
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 31 MRSCPEEQYWDPLLGTCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 20, 2005, 10:33:34 ; Search time 228 Seconds  
(without alignments)  
439.408 Million cell updates/sec

Title: US-10-618-797-2

Perfect score: 803

Sequence: 1 MRSCPEQYWAALIGTCMFC.....FPQLPPTQLSGLGNIGILL 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	196	24.4	293	2	Q53F36 HUMAN
2	195	24.3	293	1	O14836 homo sapien
3	107.5	13.4	140	2	Q5U83 MOUSE
4	107.5	13.4	249	1	Q9ET35 mus musculu
5	107.5	13.4	249	2	Q5U82 MOUSE
6	99	12.3	704	2	Q74567 TRIHA
7	98	12.2	1299	2	Q26489 SPOFR
8	97	12.1	949	2	Q5DNW1 TRINI
9	96	12.0	74	2	Q5U84 MOUSE
10	95	11.8	300	1	TNR6B HUMAN
11	94	11.7	459	2	Q62327 MOUSE
12	94	11.7	474	1	TNR1B MOUSE
13	94	11.7	474	2	Q545P4 MOUSE
14	93	11.6	5141	2	Q700K0 RAT
15	90	11.2	286	2	Q8AXC0 XENLA
16	89	11.1	1656	2	Q50S87 ENTHI
17	88.5	11.0	251	2	Q919W2 9GALL
18	88.5	11.0	862	2	Q8K071 MOUSE
19	88.5	11.0	1223	2	Q68P86 MOUSE
20	88.5	11.0	1262	2	Q80773 MOUSE
21	88.5	11.0	1675	2	Q5VL71 DROME
22	88	11.0	4010	1	FRAS1 MOUSE
23	88	11.0	4998	2	Q8CG65 MOUSE
24	87.5	10.9	724	2	Q4ZJ75 XENLA
25	87.5	10.9	729	2	Q6GPT6 XENLA
26	87	10.8	1083	2	Q51CE3 ENTHI
27	86.5	10.8	235	2	Q91YP4 MOUSE
28	86.5	10.8	1036	2	Q80T21 MOUSE
29	86	10.7	277	2	Q5T8X4 HUMAN
30	85	10.6	557	2	Q4R7B7 MACPA
31	85	10.6	589	1	GRN_MOUSE

32	85	10.6	589	2	Q544Y8 MOUSE
33	85	10.6	602	2	Q9D2V3 MOUSE
34	85	10.6	1642	2	Q515F7 ENTHI
35	84.5	10.5	596	2	Q51ZD5 MAGGR
36	84.5	10.5	1030	2	Q4FZU4 RAT
37	84.5	10.5	1061	2	Q5B110 DROME
38	84.5	10.5	1679	1	FUR2 DROME
39	84	10.5	465	2	Q7QVC3 GIALA
40	83.5	10.4	433	2	Q91ZM6 RAT
41	83.5	10.4	461	2	Q6VAU8 RAT
42	83.5	10.4	474	1	TNR1B RAT
43	83.5	10.4	474	2	Q5YLP0 RAT
44	83.5	10.4	1877	1	PCSK5 MOUSE
45	82.5	10.3	251	2	Q919X6 CENUR

# ALIGNMENTS

## RESULT 1

Q53F36\_HUMAN  
ID Q53F36 HUMAN PRELIMINARY; PRT; 293 AA.  
AC Q53F36;

DT 13-SEP-2005 (Tremblrel. 31, Created)  
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)  
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)  
DE Tumor necrosis factor receptor 13B variant (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Small intestine;

RA Maruyama K., Sugano S.;

RT "Oligo-capping: a simple method to replace the cap structure of eucaryotic mRNAs with oligoribonucleotides.";

RL Gene 138171-174 (1994).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Small intestine;

RA Suzuki Y., Yoshitomo K., Maruyama K., Sugano A., Sugano S.;

RT "Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library.";

RL Gene 200149-156 (1997).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Small intestine;

RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;

RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK223453; BAD97173.1; -; mRNA.

KW NON TER.

FT NON TER.

SQ SEQUENCE 293 AA; 31846 MW; D9EA2F28B3BF466D CRC64;

Query Match 24.4%; Score 196; DB 2; Length 293;

Best Local Similarity 27.0%; Pred. No. 1.1e-10;

Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

Qy 1 MRSCPEQYWAALIGTCMFCACICNHOSQRTCAASC-----GFWDLSPGDSVITP 51

Db 31 MRSCPEQYWDPLLTGTCMCKTICNHOSQRTCAAFCLSLCKRKEQGFYDHLRLDCTSCA 90

Qy 52 NACPQS-----TLPHSQVAERMAAGDVQ----- 76

Db 91 SICGHPKQCAFCENKLRSPVNLPELR---RQRSGEVNNSDNGRYQGLEHRSSEA 146

Qy 77 -----CGTSPSTFLWPHCLLSVSNMPCSSLPRVL----- 107

Db 147 SPALPGLKLSADQVALVYTLGLCLCAVLCAEACFLKRGDPCSCQPRSPROSPA 206

Qy 108 -----CTCSRCLCMLSIIFPQL-PPTQLSLGLP 136

```

Db      207 KSSQDHAMEAGSPVSTSPFVETCSFC-----PFECRAPTOESAVTP 248
RESULT 2
ID      TRI13B HUMAN STANDARD; PRT; 293 AA.
AC      O14836; 0726F5;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      13-SEP-2005 (Rel. 48, Last annotation update)
DE      Tumor necrosis factor receptor superfamily member 13B (Transmembrane
DE      activator and CAML interactor).
GN      Name=TNFRSF13B; Synonyms=TACI;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE (MRNA) (ISOFORM 1).
RC      TISSUE=B-cell;
RX      MEDLINE=97456245; PubMed=93111921; DOI=10.1126/science.278.5335.138;
RA      von Buelow G.-U., Bram R.J.;
RT      "NF-AT activation induced by a CAML-interacting member of the tumor
RT      necrosis factor receptor superfamily.";
RL      Science 278:138-141(1997).
RN      [2]
RP      NUCLEOTIDE SEQUENCE (MRNA) (ISOFORM 2).
RA      Zhou G., Ke R., Li H., Zheng G., Shen C., Lin L., Yang S.;
RL      Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      FUNCTION.
RX      MEDLINE=20519647; PubMed=10956646; DOI=10.1074/jbc.M005224200;
RA      Wu Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K.,
RA      Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dinko D., Lafleur D.,
RA      Migone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J.,
RA      Olson H.S., Kanakaraj P., Moore P.A., Baker K.P.;
RT      "Tumor necrosis factor (TNF) receptor superfamily member TACI is a
RT      high affinity receptor for TNF family members APRIL and BlyS.";
RL      J. Biol. Chem. 275:35478-35485(2000).
RN      [4]
RP      FUNCTION.
RX      MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;
RA      Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.,
RA      McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Scollina M.,
RA      Boyle W.J., Sarosi I., Hsu H., Snaldi G., Theilli L.E.,
RT      "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
RT      humoral immunity.";
RL      Nat. Immunol. 1:252-256(2000).
RN      [5]
RP      INTERACTIONS WITH TRAF2 AND TRAFs.
RX      MEDLINE=20341628; PubMed=10890535; DOI=10.1084/jem.192.1.137;
RA      Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
RA      Theilli L.E., Colombero A., Solovyev I., Lee F., McCabe S., Elliott R.,
RA      Miner K., Hawkins N., Guo J., Scollina M., Yu G., Wang J., Delaney J.,
RA      Meng S.-Y., Boyle W.J., Hsu H.;
RT      "TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis
RT      factor family member involved in B cell regulation.";
RL      J. Exp. Med. 192:137-143(2000).
RN      [6]
RP      X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 68-109, AND STRUCTURE BY NMR
RP      OF 68-109.
RX      PubMed=15542592; DOI=10.1074/jbc.M411714200;
RA      Hymowitz S.G., Patel D.R., Wallweber H.J., Runyon S., Yan M., Yin J.,
RA      Shriver S.K., Gordon N.C., Pan B., Skelton N.J., Kelley R.F.,
RA      Starovasnik M.A.;
RT      "Structures of APRIL-receptor complexes: like BCMA, TACI employs only
RT      a single cysteine-rich domain for high affinity ligand binding.";
RL      J. Biol. Chem. 280:7218-7227(2005).
CC      -I- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS
CC      that binds both ligands with similar high affinity. Mediates
CC      calcineurin-dependent activation of NF-AT, as well as activation

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CC      of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
CC      cell regulation and the regulation of humoral immunity.
CC      -I- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
CC      domain of CAMLG with its C-terminus.
CC      -I- INTERACTION:
CC      O75898:TNFSF13; NExp=1; IntAct=EBI-519160, EBI-519208;
CC      Q9Y275:TNFSF13B; NExp=4; IntAct=EBI-519160, EBI-519169;
CC      -I- SUBCELLULAR LOCATION: Type III membrane protein.
CC      -I- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=1;
CC      IsoId=O14836-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=O14836-2; Sequence=VSP_013798;
CC      -I- TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small
CC      intestine and peripheral blood leukocytes. Expressed in resting B-
CC      cells and activated T-cells, but not in resting T-cells.
CC      -I- SIMILARITY: Contains 2 TNFR-Cys repeats.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      EMBL; AF023614; AAC51790.1; -; mRNA.
CC      EMBL; AY302137; AAP57629.1; -; mRNA.
CC      PDB; 1XU1; X-ray; R/S/T=68-109.
CC      PDB; 1XUT; NMR; A=68-109.
CC      IntAct; O14836; -.
CC      Ensembl; ENSG00000108516; Homo sapiens.
CC      HGNC; HGNC:18153; TNFRSF13B.
CC      MIM; 604907; -.
CC      GO; GO:0005887; C-integral to plasma membrane; TAS.
CC      GO; GO:0004872; F-receptor activity; TAS.
CC      GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
CC      InterPro; IPR001368; TNFR_C6.
CC      PROSITE; PS00652; TNFR_NGFR_1; 1.
CC      PROSITE; PS00500; TNFR_NGFR_2; FALSE NEG.
CC      3D-structure; Alternative splicing; Glycoprotein; Immune response;
CC      Receptor; Repeat; Signal-anchor; Transmembrane.
CC      TOPO_DOM; 1 165 Extracellular (Potential).
CC      TRANSMEM; 166 186 Signal-anchor for type III membrane
CC      protein (Potential).
CC      REPEAT; 33 67 Cytoplasmic (Potential).
CC      REPEAT; 70 104 TNFR-Cys 1.
CC      CARBOHYD; 128 128 N-linked (GlcNAc. .) (Potential).
CC      DISULFID; 34 47 By similarity.
CC      DISULFID; 50 62 By similarity.
CC      DISULFID; 54 66 By similarity.
CC      DISULFID; 71 86 By similarity.
CC      DISULFID; 89 100 By similarity.
CC      DISULFID; 93 104 By similarity.
CC      VARSPLIC; 21 67 By similarity.
CC      -----
CC      SQ SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;
CC      FPQGLWTGVAMRSCPERQYWDPLLTGTCMCKTICNHQSORT
CC      CAAFCR -> W (in isoform 2).
CC      /FTID=VSP_013798.
CC      -----
CC      Query Match 24.3%; Score 195; DB 1; Length 293;
CC      Best Local Similarity 27.0%; Pred. No. 1.4e-11;
CC      Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;
CC      -----
CC      QY 1 MRSCPERQYWAALIGTCMFKCAICNHQSORTCAASC-----GFWDLSPGDSVITP 51
CC      DDb 31 MRSCPERQYWDPLLTGTCMCKTICNHQSORTCAAFCSLSCKRQGFYDHLRLDCISCA 90
CC      QY 52 NACPQS-----TLWPHSVAERMAAGDVQ----- 76
CC      DDb 91 SICGQHPKQCAFCNCKLRSPVNLPPELR-----QRSGEVENNSDNGRYQGLEHRSSEA 146
CC      QY 77 -----CGTSYPSFTLLWPHCLLSVSNMPCSSLPRLV----- 107

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Db 147 SPALPGLKLSADQVALVYVTLGLCLVACFLKRGKRGPCQSPRPSQSPA 206
Qy 108 -----CTCSRCRLCMLSIIFQL-PPTQLSLGP 136
Db 207 KSSQDHAMEAGSPVSPSPVETCSFC-----PPECRAPTOSSAVTP 248

RESULT 3
Q55U83_MOUSE
ID Q55U83_MOUSE PRELIMINARY; PRT; 140 AA.
AC Q55U83;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Tumor necrosis factor receptor superfamily, member 13b
DE (Fragment).
GN Name=Tnfrsf13b; ORFNames=RP23-5512.2-003;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Holt K.;
RL Submitted (PEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL646093; CA125895.1; -, Genomic DNA.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 140
SQ SEQUENCE 140 AA; 15672 MW; 005D8CDF4E8E3D15 CRC64;

Query Match 13.4%; Score 107.5; DB 2; Length 140;
Best Local Similarity 32.3%; Pred. No. 0.018;
Matches 21; Conservative 10; Mismatches 25; Indels 9; Gaps 1;

Qy 1 MRSCPQYVAALGTQWFCNAICNHSQRTCAASC-----GFWDLSQDSDVITP 51
Db 3 MAPCPQYWDSSKSCVSLTCSQSRQRTCTDFCKINCRKEQGRYYDHLGACVSCD 62

Qy 52 NACPQ 56
Db 63 STCTQ 67

RESULT 4
TR13B_MOUSE
ID TR13B_MOUSE STANDARD; PRT; 249 AA.
AC Q9ET35; Q9DBZ3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
DE activator and CAML interactor).
GN Name=Tnfrsf13b; Synonyms=faci;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=21177254; PubMed=10881172; DOI=10.1038/76889;
RA Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;
RT "Identification of a receptor for Blys demonstrates a crucial role in
RT humoral immunity.";
RL Nat. Immunol. 1:37-41(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
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RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tonaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Butt C., Hume D.A., Quackenbush J.,
RA Schiraldi L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [3]
RP FUNCTION.
RX MEDLINE=20341628; PubMed=10880535; DOI=10.1084/jem.192.1.137;
RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
RA Theill L.E., Colombero A., Solovye I., Lee P., McCabe S., Elliott R.,
RA Miner K., Hawkins N., Guo J., Stolina M., Fu G., Wang J., Delaney J.,
RA Meng S.-Y., Boyle W.J., Heu H.;
RT "TAC1 is a TRAF-interacting receptor for TALL-1, a tumor necrosis
RT factor family member involved in B cell regulation.";
RL J. Exp. Med. 192:137-143(2000).
RN [4]
RP FUNCTION.
RX MEDLINE=21322748; PubMed=11429548; DOI=10.1038/89782;
RA Wang H., Marsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,
RA Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.;
RT "TAC1-ligand interactions are required for T cell activation and
RT collagen-induced arthritis in mice.";
RL Nat. Immunol. 2:632-637(2001).
CC -1- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAPF/BLYS
CC that binds both ligands with similar high affinity. Mediates
CC calcineurin-dependent activation of NF-AT, as well as activation
CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
CC cell function and the regulation of humoral immunity (By
CC similarity).
CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
CC domain of CAMLG with its C-terminus (By similarity).
CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC -1- SIMILARITY: Contains 2 TNFR-Cys repeats.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF257673; AAC00081.1; -, mRNA.
CC EMBL; AK004668; BAB23457.1; -, mRNA.
CC Ensembl; ENSMUSG0000010142; Mus musculus.
CC MGI; MGI:1899411; Tnfrsf13b.
CC GO; GO:0009897; C:external side of plasma membrane; IDA.
CC GO; GO:0005887; C:integral to plasma membrane; IDA.
CC GO; GO:0001782; P:B cell homeostasis; IMP.
CC GO; GO:0030889; P:negative regulation of B cell proliferation; IMP.
CC InterPro; IPR001368; TNFR c6.
CC PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
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```
DR PROSITE; PS0050; TNFR_NGFR_2; FALSE NEG.
KW Immune response; Receptor; Repeat; Signal-anchor; Transmembrane.
FT TOPO_DOM 1 128 Extracellular (Potential).
FT TRANSMEM 129 149 Signal-anchor for type.III membrane
FT protein (Potential).
FT TOPO_DOM 150 249 Cytoplasmic (Potential).
FT REPEAT 5 38 TNFR-Cys 1.
FT REPEAT 42 76 TNFR-Cys 2.
FT DISULFID 6 19 By similarity.
FT DISULFID 22 34 By similarity.
FT DISULFID 26 38 By similarity.
FT DISULFID 43 58 By similarity.
FT DISULFID 61 72 By similarity.
FT DISULFID 65 76 By similarity.
FT CONFLICT 137 137 I -> F (in Ref. 2).
SQ SEQUENCE 249 AA; 26947 MW; CB2F2D61C2931D81 CRC64;

Query Match 13.4%; Score 107.5; DB 1; Length 249;
Best Local Similarity 32.3%; Pred. No. 0.033;
Matches 21; Conservative 10; Mismatches 25; Indels 9; Gaps 1;

QY 1 MRSPCEQYWAALLGTCMFCFCAICNHQSQRTCAASC-----GEFWDLSPGDSVITP 51
DQ 3 MAFCPKQYWDSSRKSCVSCALTCQSQRSTCTDFCFKFNCRKEQGRYYDHLGACVSCD 62
QY 52 NACPQ 56
DQ 63 STCTQ 67

RESULT 5
Q5SU82 MOUSE PRELIMINARY; PRT; 249 AA.
AC Q5SU82;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Tumor necrosis factor receptor superfamily, member 13b.
GN Name=TNFRsf13b; ORFNames=RP23-5512.2-001;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Holt K.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL646093; CAI25896.1; -; Genomic_DNA.
KW Receptor.
SQ SEQUENCE 249 AA; 26947 MW; CB2F2D61C2931D81 CRC64;

Query Match 13.4%; Score 107.5; DB 2; Length 249;
Best Local Similarity 32.3%; Pred. No. 0.033;
Matches 21; Conservative 10; Mismatches 25; Indels 9; Gaps 1;

QY 1 MRSPCEQYWAALLGTCMFCFCAICNHQSQRTCAASC-----GEFWDLSPGDSVITP 51
DQ 3 MAFCPKQYWDSSRKSCVSCALTCQSQRSTCTDFCFKFNCRKEQGRYYDHLGACVSCD 62
QY 52 NACPQ 56
DQ 63 STCTQ 67

RESULT 6
O74567 TRIHA PRELIMINARY; PRT; 704 AA.
AC O74567;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Q174 protein.
KW Receptor.
SQ SEQUENCE 704 AA; 77925 MW; 53414BDDC365EBC CRC64;

Query Match 12.3%; Score 99; DB 2; Length 704;
Best Local Similarity 22.1%; Pred. No. 0.63;
Matches 32; Conservative 14; Mismatches 37; Indels 62; Gaps 8;

QY 3 SCPEEQYWAALLGTCMFCFCAICNHQSQRTCAASC-----GEFWDLSPGDSVITP 51
DQ 508 SCPDSQYWDGSKCACPFGTWDGKHCHNQGDKAHFDSNKKQKQGEVYDSKSKTCS 567
QY 34 ASCGEFWDLSPGDSVITPACPOSTLWPHSQVAERMAGDVQCG--TSYPTSTFLWPHC 91
DQ 568 CPDQYWDGS-----KCACPVGKVDGKQCVF-----NCGKDAVSYS----- 604
QY 92 LLSVSNMPCSSLPRVL-----CTC 110
DQ 605 --KQKNCVCKNIGQVDFTKSLTCS 627

RESULT 7
Q26489 SPOFR PRELIMINARY; PRT; 1299 AA.
AC Q26489;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Endoprotease FURIN.
GN Name=FURIN;
OS Spodoptera frugiperda (Fall armyworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Amphipyrinae; Spodoptera.
OX NCBI_TaxID=7108;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cleplik M., Klenk H.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z68888; CAA93116.1; -; mRNA.
DR PIR; T43251; T43251.
DR HSSP; P23188; 1P8J.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR InterPro; IPR006212; Furin repeat.
DR InterPro; IPR000209; Pept_58_S53.
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DR InterPro; IPR002884; P:protnconvertap.
DR Pfam; PF01483; P:proteins; 1.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR SMART; SM00261; FU; 10.
DR PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN_1.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Protease.
SQ SEQUENCE 1299 AA; 142020 MW; 4C3799C7B5C572AB CRC64;

Query Match 12.2%; Score 98; DB 2; Length 1299;
Best Local Similarity 25.9%; Pred. No. 1.5;
Matches 36; Conservative 15; Mismatches 58; Indels 30; Gaps 7;

Qy 1 MRSCPQYVAALGTCTCFKCAICNHQSORT--CAASGGEFWDLSPGDSVITPACPOSTL 58
Db 781 LQQCPDGYDESSVCRPAAHCAATCSDRADGC-TSCHEHLVLHDTGTCMA---SCPPS- 835
Qy 59 LWPHSQVAERMA-----GGDVQCGTSYSPFLWPHCLLSV-----SNMP 99
Db 836 ---HYETEDYMCACHESCDTCGSGEACQVCTCHPSTVALDGRCTVSCPSGYADKKRKE 892
Qy 100 CSSLPRLVLTCCSR-CLEC 117
Db 893 CMRCFVGCSTCTSAFCLSC 911

RESULT 8
QSDNW1 TRINI PRELIMINARY; PRT; 949 AA.
AC QSDNW1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Furin-like convertase.
OS Trichoplusia ni (Cabbage looper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Plusiinae; Trichoplusia.
OX NCBI_TaxID=7111;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wang L., Yang G., Wu X.;
RT "Cloning, expression, and characterization of recombinant Tn5 cells
RT furin-like convertase from baculovirus-infected insect cells.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY555267; AAT37510.1; -; mRNA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006212; Furin repeat.
DR InterPro; IPR002884; P:protnconvertap.
DR Pfam; PF01483; P:proteins; 1.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PRODOM; PD000717; P:protnconvertap; 1.
DR SMART; SM00261; FU; 5.
DR PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN_1.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
SQ SEQUENCE 949 AA; 104439 MW; 32C4731E491F968C CRC64;

Query Match 12.1%; Score 97; DB 2; Length 949;
Best Local Similarity 25.9%; Pred. No. 1.3;
Matches 36; Conservative 13; Mismatches 60; Indels 30; Gaps 7;

Qy 1 MRSCPQYVAALGTCTCFKCAICNHQSORT--CAASGGEFWDLSPGDSVITPACPOSTL 59
Db 781 LQQCPDGYDESSVCRPAAHCAATCSDRADGC-TSCHEHLVLHDTGTCMA---SCPPS- 835
Qy 60 WPHSQVAERMA-----GGDVQCGTSYSPFLWPHCLLSV-----SNMPC 100

Db 836 --HYETEDYMCACHESCDTCGSGEACQVCTCHPSTVALDGRCTVSCPSGYADKKRKE 893
Qy 101 SSLPRLVLTCCSR--CLEC 117
Db 894 MRCP-VGCASCTSAFCLSC 911

RESULT 9
QSSU84 MOUSE PRELIMINARY; PRT; 74 AA.
AC QSSU84;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Tumor necrosis factor receptor superfamily, member 13b
DE (Fragment).
GN Names=TNFRsf13b; ORFNames=RP23-5512.2-002;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Holt K.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL646093; CAI25894.1; -; Genomic DNA.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 74
SQ SEQUENCE 74 AA; 8337 MW; DA8A3B06FE191A26 CRC64;

Query Match 12.0%; Score 96; DB 2; Length 74;
Best Local Similarity 41.7%; Pred. No. 0.12;
Matches 15; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MRSCPQYVAALGTCTCFKCAICNHQSORTCAASC 36
Db 3 MAFCKDDQYWDSSKSCVSCALTCQSQRSTCTDFC 38

RESULT 10
TNR6B HUMAN STANDARD; PRT; 300 AA.
AC OS5407;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6B precursor (Decoy
DE receptor for Fas ligand) (Decoy receptor 3) (DCR3) (M68).
GN Name=TNFRSF6B; Synonyms=DCR3, TR6; ORFNames=UNQ186/PRO212;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Fetal lung;
RX MEDLINE=99087326; PubMed=9872321; DOI=10.1038/25387;
RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel P.C.,
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
RA Godowski P.J., Wood W.I., Gurney A.H., Hillan K.J., Cohen R.L.,
RA Goddard A.D., Botstein D., Ashkenazi A.;
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
RT colon cancer.";
RL Nature 396:699-703 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 30-35.
RC TISSUE=Prostate;
RX MEDLINE=99253915; PubMed=10318773; DOI=10.1074/jbc.274.20.13733;
RA Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;

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RT "A newly identified member of tumor necrosis factor receptor  
 RT superfamily (TRF) suppresses LIGHT-mediated apoptosis.";  
 RL J. Biol. Chem. 274:13733-13736(1999).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=20122600; PubMed=10655513; DOI=10.1073/pnas.97.3.1230;  
 RA Bai C., Connolly B., Metzger M.L., Hilliard C.A., Liu X., Sandig V.,  
 RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;  
 RT "Overexpression of M68/Dc3 in human gastrointestinal tract tumors  
 RT independent of gene amplification and its location in a four-gene  
 RT cluster.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
 RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,  
 RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
 RA Vandien R.L., Watanabe C., Weand D., Woods K., Xie M.-H., Goddard A.D.,  
 RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,  
 RA Wood W.I., Godowski P.J., Gray A.M.;  
 RT "The secreted protein discovery initiative (SPDI), a large-scale  
 RT effort to identify novel human secreted and transmembrane proteins: a  
 RT bioinformatics assessment.";  
 RL Genome Res. 13:2265-2270(2003).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;  
 RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,  
 RA Bailey J., Barlow K.P., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 RA Cuslton A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Grafham D.V., Griffiths J.C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Lehesvalho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConnachie L.J., McIay C., McMurray A.A.,  
 RA Milne S.A., Mistry A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,  
 RA Stuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:865-871(2001).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC TISSUE=Lung, and Skin;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Haie S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Maman A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Decoy receptor for the cytotoxic ligands TNFS14/LIGHT  
 CC and TNFS6/FASL. Protects against apoptosis.  
 CC -1- INTERACTION:  
 CC O43557:TNFSF14; NDEXP=1; IntAct=EBI-524171, EBI-524131;  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.  
 CC Detected in adult stomach, spinal cord, lymph node, trachea,  
 CC spleen, colon and lung. Highly expressed in several primary tumors  
 CC from colon, stomach, rectum, esophagus and in SW480 colon  
 CC carcinoma cells.  
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR ENBL; AF104419; AAD03056.1; -; mRNA.  
 DR ENBL; AF134240; AAD29688.1; -; mRNA.  
 DR ENBL; AF217796; AAF35244.1; -; Genomic\_DNA.  
 DR ENBL; AF217793; AAF33685.1; -; mRNA.  
 DR ENBL; AF217794; AAF33686.1; -; mRNA.  
 DR ENBL; AV358279; AAQ88646.1; -; mRNA.  
 DR ENBL; AL121845; AAC03668.1; -; Genomic\_DNA.  
 DR ENBL; BC017065; AAH17065.1; -; mRNA.  
 DR ENBL; BC034349; AAH34349.1; -; mRNA.  
 DR HSSP; O14763; 1DU3.  
 DR Ensembl; O95407; -;  
 DR Ensembl; ENSG00000026036; Homo sapiens.  
 DR HGNC; HGNC:11921; TNFRSF6B.  
 DR H-InvDB; HIX0016007; -;  
 DR MIM; 603361; -;  
 DR GO; GO:0005625; C:soluble fraction; TAS.  
 DR GO; GO:0004872; F:receptor activity; TAS.  
 DR GO; GO:0006916; P:anti-apoptosis; TAS.  
 DR InterPro; IPR001368; TNFR\_C6.  
 DR Pfam; PF00020; TNFR\_C6; 2.  
 DR SMART; SM00208; TNFR; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 KW Apoptosis; Direct protein sequencing; Glycoprotein; Receptor; Repeat;  
 KW Signal.  
 FT SIGNAL  
 FT CHAIN 1 29 Tumor necrosis factor receptor  
 FT CHAIN 30 30 superfamily member 6B.  
 FT REPEAT 31 70 TNFR-Cys 1.  
 FT REPEAT 72 113 TNFR-Cys 2.  
 FT REPEAT 115 150 TNFR-Cys 3.  
 FT REPEAT 152 193 TNFR-Cys 4.  
 FT REPEAT 173 173 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 49 62 By similarity.  
 FT DISULFID 52 70 By similarity.  
 FT DISULFID 73 88 By similarity.  
 FT DISULFID 91 105 By similarity.  
 FT DISULFID 95 113 By similarity.  
 FT DISULFID 115 126 By similarity.  
 FT DISULFID 132 150 By similarity.  
 FT DISULFID 133 168 By similarity.  
 FT DISULFID 174 193 By similarity.  
 SQ SEQUENCE 300 AA; 32680 MW; F90AE33718449AF CRC64;  
 Query Match 11.8%; Score 95; DB 1; Length 300;

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Best Local Similarity 25.2%; Pred. No. 0.63;
Matches 36; Conservative 9; Mismatches 46; Indels 52; Gaps 7;

Qy 4 CPBE---QYRAALGTCHFKCAICNHSQ--RTCAAS-----CGEFWD 41
Db 73 CPPHYTQFW-NYLERYCYNVLCGEREEARACHATHNACRACRTGFFAHAGFCLSHAS 131
Qy 42 LSPGDSVITPNACQSTLWPHSQAVERMAGDVQCGTSVPSTF-----LLWPH--- 90
Db 132 CPGAGVIAPTPQNT-----QCQPCPGTFSASSSSSEQCQPHNC 174
Qy 91 -CLLSVSNMPCSSPRVLCTCCS 112
Db 175 TALGLALNVPGSSHDTLCTST 197

RESULT 11
Q62327 MOUSE
ID Q62327 MOUSE PRELIMINARY; PRT; 459 AA.
AC Q62327;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tumour necrosis factor receptor 2 protein (fragment).
GN Name=Tnfrsf1b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Amino acid variation in the tumor Necrosis factor receptor 2 is
RT linked to autoimmune diabetes in NOD mice.";
RL Genomics 0:0(0).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Allelic variation of the type 2 tumor necrosis factor receptor
RT gene.";
RL Mamm. Genome 5:726-727(1994).
DR EMBL; X76401; CAA53981.1; -; mRNA.
DR PIR; I48854; I48854.
DR HSSP; P19438; INCF.
DR MGI; MGI:1314883; Tnfrsf1b.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005031; F:tumor necrosis factor receptor activity; IEA.
DR GO; GO:0019221; P:cytokine and chemokine mediated signaling p...; IEA.
DR InterPro; IPR013366; TNFRcpt 2.
DR InterPro; IPR013368; TNFR c6.
DR Pfam; PF00020; TNFR_c6_2.
DR PIRSF; PIRSF001968; TNFR_2; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER.
SQ SEQUENCE 459 AA; 48686 MW; 6C51D2CF1C4626DF CRC64;

Query Match 11.7%; Score 94; DB 2; Length 459;
Best Local Similarity 24.2%; Pred. No. 1.2;
Matches 36; Conservative 17; Mismatches 64; Indels 32; Gaps 6;

Qy 16 TCMECKA-----ICNHSQRTCAASCGEFWDLSPGDSVITPNACQ-----STLWP 61
Db 78 TCLSCSSCSCTDQVETRACTKQQRVCAAGRYCALKTHS-----GSCRQCMRLSKGP 132
Qy 62 HSQVAERMAGDVQCGTSVPSTF-----LLWPHCLLSVSNMPCSSLPVLCTCCSR 113

us-10-618-797-2.rup

Db 133 GFGVASSRAENGVLKACAPGTFSDTTSVDCRPHRICSLAIPGNASTDAVCAPESP 192
Qy 114 CLSCMLSIIPQLP-PTQLSGL-----GPN 137
Db 193 TLSAIPRTLXVSQPEPTRSQPLDQEPGFS 221

RESULT 12
TNFR1B MOUSE
ID TNFR1B MOUSE STANDARD; PRT; 474 AA.
AC P25119; O88734; P97893;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Tumour necrosis factor receptor superfamily member 1B precursor (Tumor
DE necrosis factor receptor 2) (TNF-R2) (Tumor necrosis factor receptor
DE type II) (p75) (p80 TNF-alpha receptor).
GN Name=Tnfrsf1b; Synonyms=Tnfr-2, Tnfr2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=91187885; PubMed=1849278;
RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H.,
RA Chen E.Y., Goeddel D.V.;
RT "Cloning and expression of cDNAs for two distinct murine tumor
RT necrosis factor receptors demonstrate one receptor is species
RT specific.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=91246168; PubMed=1645445;
RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA Copeland N.G., Jenkins N.A., Smith C.A.;
RT "Molecular cloning and expression of the type 1 and type 2 murine
RT receptors for tumor necrosis factor.";
RL Mol. Cell. Biol. 11:3020-3028(1991).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=98414512; PubMed=9740674; DOI=10.1006/geno.1998.5407;
RA Hurler B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
RT "The mouse tumor necrosis factor receptor 2 gene: genomic structure
RT and characterization of the two transcripts.";
RL Genomics 52:79-98(1998).
RN [4]
RP NUCLEOTIDE SEQUENCE OF 1-26.
RC STRAIN=NOD;
RA Jacob C.O., Liu J.;
RT Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE OF 1-22.
RC TISSUE=Liver;
RA Kissnerghis M., Fellows R., Feldmann M., Chernajovsky Y.;
RT Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and
CC approximately 5-fold lower affinity for homotrimeric
CC TNFSF1/lymphotoxin-alpha. The TRAF1/TRAFA2 complex recruits the
CC apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2 (By
CC similarity).
CC -1- SUBUNIT: Binds to TRAF2 (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
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Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L.,  
 Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 Miyazaki A., Sakai K., Sakai D., Shibata K., Shinagawa A.,  
 Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 Birney E., Hayashizaki Y.;  
 "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs";  
 Nature 420:563-573(2002).  
 [4]  
 NUCLEOTIDE SEQUENCE.  
 STRAIN=C57BL/6J; TISSUE=Liver, and Lung;  
 MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 "Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes";  
 Genome Res. 10:1617-1630(2000).  
 [5]  
 NUCLEOTIDE SEQUENCE.  
 STRAIN=C57BL/6J; TISSUE=Liver, and Lung;  
 MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,  
 Konno H., Akiyama J., Nishi K., Kitsuani T., Tashiro H., Itoh M.,  
 Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;  
 "RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer";  
 Genome Res. 10:1757-1771(2000).  
 [6]  
 NUCLEOTIDE SEQUENCE.  
 STRAIN=C57BL/6J; TISSUE=Liver, and Lung;  
 Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
 Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
 Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
 Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
 Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
 Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
 Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,  
 Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,  
 Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
 Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
 Muramatsu M., Hayashizaki Y.;  
 Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 EMBL; AK004844; BAB23610.1; -; mRNA.  
 EMBL; AK004752; BAB23533.1; -; mRNA.  
 MG1; MG1:1314883; Thirslb.  
 GO; GO:0005615; C:extracellular space; TAS.  
 GO; GO:0016021; C:integral to membrane; TAS.  
 GO; GO:0008219; P:cell death; IMP.  
 GO; GO:0008283; P:cell proliferation; TAS.  
 GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; IMP.  
 GO; GO:0006954; P:inflammatory response; IMP.  
 KW Receptor.  
 SQ SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;  
 Query Match 11.7%; Score 94; DB 2; Length 474;  
 Best Local Similarity 24.2%; Pred. No. 1.3;  
 Matches 36; Conservative 17; Mismatches 64; Indels 32; Gaps 6;  
 16 TCMFCKA-----ICNHQSORTCAASGCEFWDLSPGDSVITPNACPO-----STLWP 61  
 93 TCLSCSSSTTDQVEIRACTQQRNVCAACEGRYCALKTHS-----GSCQCKRLSKGP 147  
 62 HSQVAERMAAGDVGQCTSYSTF-----LWPHCLLSVSNMPCSSIPRLVCTCCSR 113  
 148 GFGVASSRAPNGVNLKACAPGTFTSDTTSSTDCRPHRISILAIIPGNASTDAVCAPEP 207

114 CLSCMLSIIPQLP-PTOLSGL----GPN 137  
 208 TLSAIPRTLVVSQPEPTRSQPLDQEPGPS 236  
 RESULT 14  
 Q700K0 RAT PRELIMINARY; PRT; 5141 AA.  
 ID Q700K0 RAT PRELIMINARY; PRT; 5141 AA.  
 AC Q700K0 RAT PRELIMINARY; PRT; 5141 AA.  
 DT 03-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE SCO-spondin.  
 GN Names=sco-spondin;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Meinel O.;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 RE EMBL; AJ629845; CAF33425.1; -; mRNA.  
 DR HSP; P01130; IAJJ.  
 GO; GO:0007155; P:cell adhesion; IEA.  
 DR InterPro; IPR006207; Cys\_knot\_C.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR011489; EMI.  
 DR InterPro; IPR000421; FAS8\_C.  
 DR InterPro; IPR001545; Gly\_hormoneB.  
 DR InterPro; IPR002172; LDL\_receptor\_A.  
 DR InterPro; IPR02919; Pro\_inh\_CR\_Til.  
 DR InterPro; IPR000884; TSPI.  
 DR InterPro; IPR006552; VWC\_out.  
 DR InterPro; IPR001007; VWF\_C.  
 DR InterPro; IPR001846; VWF\_D.  
 DR Pfam; PF07546; EMI; 1.  
 DR Pfam; PF00754; F5\_F8\_type\_C; 1.  
 DR Pfam; PF00057; Ldl\_recept\_a; 10.  
 DR Pfam; PF01826; TIL; 12.  
 DR Pfam; PF00090; TSP; 1; 24.  
 DR Pfam; PF00093; VWC; 1.  
 DR Pfam; PF00094; VWD; 3.  
 DR PRINTS; PR00261; LDLRECEPTOR.  
 DR SMART; SM00192; Ldla; 10.  
 DR SMART; SM00209; TSPI; 25.  
 DR SMART; SM00214; VWC; 5.  
 DR SMART; SM00215; VWC\_out; 9.  
 DR SMART; SM00216; VWD; 3.  
 DR PROSITE; PS01235; CTCK\_2; 1.  
 DR PROSITE; PS01186; EGF\_3; 1.  
 DR PROSITE; PS00022; FAS8C\_3; 1.  
 DR PROSITE; PS00261; GLYCO\_HORMONE\_BETA\_1; UNKNOWN\_2.  
 DR PROSITE; PS01209; LDLRA\_1; 8.  
 DR PROSITE; PS00068; LDLRA\_2; 10.  
 DR PROSITE; PS00092; TSPI\_24.  
 DR PROSITE; PS01208; VWF\_C\_1; UNKNOWN\_1.  
 DR PROSITE; PS0184; VWF\_C\_2; 2.  
 DR PROSITE; PS0184; VWF\_C\_2; 2.  
 SQ SEQUENCE 5141 AA; 550644 MW; 1772AB67F02C5E3 CRC64;  
 Query Match 11.6%; Score 93; DB 2; Length 5141;  
 Best Local Similarity 26.0%; Pred. No. 18;  
 Matches 40; Conservative 11; Mismatches 43; Indels 60; Gaps 11;  
 4 CPBEQWAAALGTC-MFCKAICNHQSORT-----CAASGCEFWDLSPGDSV-----IT 50  
 4814 CPFGQ----VLSTCATICPSFCSHLWPGTICVREPCQLGCG-----CPGQLLHSGTCIP 4864  
 51 PNCAPSTL---W-----PHSQVAERMAAGDVGQCTSYSTFLLW---PHCLLSVSNMPCS 101  
 4865 PEACPCTRLSLPGLTLPLEEAQELPSG-----TVLTWNCTHCTCQGGVFTCS 4913

Qy 102 SLPRVLCTCSRCLCMLSIIFPOLPPTQLSGLG 135  
Db 4914 H-----TDCQEC-----PGEILQLG 4929

## RESULT 15

Q8AXCO XENLA  
ID Q8AXCO XENLA PRELIMINARY; PRT; 286 AA.  
AC Q8AXCO;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Riddle 4.  
GN Name=Rdd4;  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP NUCLEOTIDE SEQUENCE  
RA Wardle F.C., Sive H.L.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF465788; AA015689.1; -; mRNA.  
DR HSSP; P56682; ICCV.  
DR InterPro; IPR002919; Prot\_Inh\_CR\_TIL.  
DR Pfam; PF01826; TIL; 4.  
SQ SEQUENCE 286 AA; 31037 MW; 9C2DAB2E975DCE73 CRC64;

Query Match 11.2%; Score 90; DB 2; Length 286;  
Best Local Similarity 25.6%; Pred. No. 1.8;  
Matches 40; Conservative 13; Mismatches 59; Indels 44; Gaps 9;

Qy 4 CPPEQYWAALLGTC-MECK-----AICNHQSORTCAASCGEFWDLSPGDS--VITPNAC 54  
Db 29 CAPNQVWNSCGTACPLNCQFNRPDPDVCILSCQRC--FCKEPIYFQNGDSGPCVLPSQC 86  
Qy 55 POSTLWPHSQVAERWAGGV--CCGTSPSTFLWPHCLLSVNMPCSSLPRVLCTCCS 112  
Db 87 PPSQV-----ESCAPNQVWNSCGTA-----CPLNCQNF--RNPPDVCILSCQ 126  
Qy 113 RCLCMLSIIF-----POLPPTQLSGLGPN 137  
Db 127 RGCFCKEPIYFQNGTSGPCVLPSCPPSQVESCAPN 162

Search completed: December 20, 2005, 10:42:47  
Job time : 231 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 20, 2005, 10:33:34 ; Search time 38 seconds  
(without alignments)  
359.547 Million cell updates/sec

Title: US-10-618-797-2

Perfect score: 803

Sequence: 1 MRSCPEEQYWAALLGTCMFC.....FPQLPPTQLSLGPNIGGLL 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_80.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	12.2	1299	2 T43251	furin (EC 3.4.21.75)
2	94	11.7	459	2 I48854	gene murine tumour
3	94	11.7	474	2 B38634	tumor necrosis fac
4	85	10.6	589	2 C38128	epithelin/granulin
5	84.5	10.5	1680	2 A43434	furin (EC 3.4.21.7
6	83.5	10.4	1548	2 S34583	serine proteinase
7	81	10.1	250	1 A49053	CD27 antigen precu
8	80.5	10.0	593	1 GYHU	granulin precursor
9	80	10.0	349	2 T43457	hypothetical prote
10	79.5	9.9	1700	2 S08167	Balbani ring 3 pr
11	78.5	9.8	1373	2 JE0095	gastric mucin MUC5
12	77.5	9.7	2219	2 T27684	hypothetical prote
13	77	9.6	981	2 S51604	receptor-like tyro
14	77	9.6	1005	2 S49015	receptor tyrosine
15	76.5	9.5	355	2 S64445	polyferredoxin 4x2
16	76.5	9.5	589	2 B38128	epithelin/granulin
17	75.5	9.4	732	1 MNXRW4	nonstructural prot
18	74.5	9.3	591	2 I48141	acroganin - guine
19	74.5	9.3	5376	2 T42215	zonaladhesin - mou
20	73.5	9.2	810	2 T10756	Nei-nomolog protei
21	73.5	9.2	1737	2 T05029	MEGF8 protein - hu
22	73.5	9.2	2871	2 A55624	fibrillin-1 precu
23	73	9.1	230	2 A38346	ultra-high-sulfur
24	73	9.1	260	1 A46517	CD27 antigen precu
25	73	9.1	337	2 I47079	folliculin - shee
26	73	9.1	344	2 I45894	folliculin - bovi
27	73	9.1	991	2 I78843	receptor protein-t
28	72.5	9.0	265	2 T33695	hypothetical prote
29	72	9.0	546	2 T46718	probable farneysl

30	72	9.0	1827	2 T34288	hypothetical prote
31	71.5	8.9	1115	2 T11614	probable poly(A)-s
32	71.5	8.9	2155	2 T30197	alpha tectorin - m
33	71	8.8	907	2 T27317	hypothetical prote
34	70.5	8.8	264	2 T47183	hypothetical prote
35	70.5	8.8	417	2 T25050	hypothetical prote
36	70.5	8.8	532	2 T04748	hypothetical prote
37	70.5	8.8	835	2 JP0076	nei protein - chic
38	70	8.7	223	2 B38346	ultra-high-sulfur
39	70	8.7	1642	2 T19130	hypothetical prote
40	70	8.7	2195	2 T34264	hypothetical prote
41	70	8.7	2761	2 T21064	hypothetical prote
42	70	8.7	3002	2 A47221	fibrillin 1 precu
43	69.5	8.7	480	2 S52306	zinc finger protei
44	69.5	8.7	518	2 B86299	hypothetical prote
45	69.5	8.7	654	2 T30136	hypothetical prote

## ALIGNMENTS

### RESULT 1

T43251

furin (EC 3.4.21.75) - fall armyworm

N;Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serine

C;Species: Spodoptera frugiperda (fall armyworm)

C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004

C;Accession: T43251

R;Cleplink, M.; Klenk, H.

submitted to the EMBL Data Library, January 1996

A;Description: Cloning and functional characterization of FURIN from Spodoptera frugiperda

A;Reference number: Z22368

A;Accession: T43251

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1299 <CIE>

A;Cross-references: UNIPROT:Q26489; UNIPARC:UPI0000083055; EMBL:Z68888; NID:gl167859; PIR

A;Experimental source: clone Sfurin 6; ovary

C;Function:

A;Description: responsible for the endoproteolytic processing of proproteins with specific

C;Keywords: hydrolase; serine proteinase

Query Match	12.2%	Score 98;	DB 2;	Length 1299;
Best Local Similarity	25.9%	Pred. No. 0.44;		
Matches	36;	Conservative	15;	Mismatches 58; Indels 30; Gaps 7;
QY	1	MRSCPEEQYWAALLGTCMFC	KAICNHQSORT--CAASCGEFNDLSPGDSVITNACPQST	58
Db	781	LQCCPDGYWEDSEASVCRP	CAAHCAATCSEADGC-TSC	EHHLVLDHGTGNA---SCPPS- 835
QY	59	LWPHSQVAERMA-----	GGDVCGTSYPTFTLLMPHCLLSV-----	SNMP 99
Db	836	---HYETEDDMCAKHESCD	TGCGPGETQCVTSTYALDGR	CVTSCPPAYYADKKRKE 892
QY	100	CSSLPRVLCTCCSR-CLEC	117	
Db	893	CMRCPVGCSTCTSAFCLSC	911	

### RESULT 2

I48854

gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C;Accession: I48854

R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.

Mamm. Genome 5, 726-727, 1994

A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.

A;Reference number: I48854; MUID:95178848; PMID:7873884

A;Accession: I48854

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-459 <RES>



A43434  
Eumecurus (EC 3.4.21.75) 2 - fruit fly (Drosophila melanogaster)

RESULT 5  
A43434  
furin (EC 3.4.21.75) 2 - fruit fly (*Drosophila melanogaster*)  
C:Species: *Drosophila melanogaster*



C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A43434  
R;Roebroek, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, E.  
J. Biol. Chem. 267, 17208-17215, 1992  
A;Title: Cloning and functional expression of Dfurin2, a subtilisin-like proprotein proc  
A;Reference number: A43434; MUID:92381036; PMID:1512259  
A;Accession: A43434  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1680 <ROE>  
A;Cross-references: UNIPROT:P30432; UNIPARC:UPI000016BC03; GB:M94375; NID:G157461; PID:9  
A;Note: sequence extracted from NCBI backbone (NCBIN:111933, NCBI:P111934)  
C;Genetics:  
A;Gene: FlyBase:Fur2  
A;Cross-references: FlyBase:FBgn0004598  
C;Keywords: hydrolase; serine proteinase; transmembrane protein  
F;409-652/Domain: subtilisin homology <SBT>  
F;418,457,638/Active site: Asp, His, Ser #status predicted

Query Match 10.5%; Score 84.5; DB 2; Length 1680;  
Best Local Similarity 28.3%; Pred. No. 8.9;  
Matches 32; Conservative 14; Mismatches 40; Indels 27; Gaps 6;

Qy 4 CPEQYWAALLGTCMFKCAICNHQSQRTCAASCGEFDLSPGDSVITPNACPOSTLWPHS 63  
Db 1199 CSESEFYQVEGQC-----RPCHASGSC--NGPADTSC--SCPPNRLLEQS 1242  
Qy 64 QVAERAGGVDQCTGTPSTFLLWPHCLLSVSNMPCSSLPRLVCTCCSCLE 116  
Db 1243 RCVSGREGFPVEAGS-----LCSPCLHTCSQ--CVS--RTNCSNCSRGLE 1284

RESULT 6  
S34583  
serine proteinase (BC 3.4.21.-) PC6B - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C;Accession: S34583  
R;Nakagawa, T.; Murakami, K.; Nakayama, K.  
FEBS Lett. 327, 165-171, 1993  
A;Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a  
A;Reference number: S34583; MUID:93327934; PMID:8335106  
A;Accession: S34583  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1548 <NAK>  
A;Cross-references: UNIPROT:Q04592; UNIPARC:UPI000016CF9E; GB:D17583; NID:G407344; PIDN:  
C;Keywords: hydrolase; serine proteinase

Query Match 10.4%; Score 83.5; DB 2; Length 1548;  
Best Local Similarity 29.3%; Pred. No. 10;  
Matches 39; Conservative 5; Mismatches 52; Indels 37; Gaps 9;

Qy 3 SCPEQYWAALLGTCMFKCAICNHQSQRTCAASCGEFDLSPGDSVITPNACPOSTL 59  
Db 963 SCPEGFY--AKDGVCEHCSSPC-----KTEGNATSCNS---CEGDFVLDHGVGVC----- 1006  
Qy 60 W----PHSQVAERWAG-----GDVCGTSTPSTFLLWPHCLLSVSNMPCSSLP-- 104  
Db 1007 WKTCPKPKHVAVEGCKRCPQCQDIHKTCKECPDPFFLYNDMCHRS-----CPKSFYPM 1063  
Qy 105 RVLCTCCSRLEC 117  
Db 1064 RQVPCCHNCLC 1076

RESULT 7  
A49053  
CD27 antigen precursor - mouse  
N;Alternate names: CD27L receptor; T cell activation antigen CD27  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Dec-1993 #sequence\_revision 22-Apr-1995 #text\_change 09-Jul-2004  
C;Accession: A49053

R;Graveststein, L.A.; Blom, B.; Nolten, L.A.; de Vries, E.; van der Horst, G.; Ossendorp, E.  
Eur. J. Immunol. 23, 943-950, 1993  
A;Title: Cloning and expression of murine CD27: comparison with 4-1BB, another lymphocyte  
A;Reference number: A49053; MUID:93209296; PMID:8384562  
A;Accession: A49053  
A;Molecule type: mRNA  
A;Residues: 1-250 <GRA>  
A;Cross-references: UNIPROT:P41272; UNIPARC:UPI0000023489  
A;Note: sequence extracted from NCBI backbone (NCBIN:128168, NCBI:P128169)  
C;Superfamily: CD27 antigen; NGF receptor repeat homology  
C;Keywords: duplication; glycoprotein; homodimer; receptor; surface antigen; T-cell; tra  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-250/Product: CD27 antigen #status predicted <NAT>  
F;21-182/Domain: extracellular #status predicted <EXT>  
F;27-63/Domain: NGF receptor repeat homology <NG1>  
F;65-105/Domain: NGF receptor repeat homology <NG2>  
F;121-179/Region: proline/serine/threonine-rich  
F;183-202/Domain: transmembrane #status predicted <TMN>  
F;203-250/Domain: intracellular #status predicted <INT>  
F;95,162/Binding site: carbohydrate (Asn) #status predicted

Query Match 10.1%; Score 81; DB 1; Length 250;  
Best Local Similarity 20.7%; Pred. No. 3.6;  
Matches 35; Conservative 12; Mismatches 46; Indels 76; Gaps 9;

Qy 9 YWAALLGTCMFKCAICNHQSQRTCAASCGEFDLSPGDSVITPNACPOSTLWPHSQA-- 66  
Db 7 YWLCMLGTLVLSA-----TLAPNSCDPKHYWTGGGLCCR 41  
Qy 67 -----EERMAGGDVQC-----GTSYPTSTFLLWPHCL-----LSVSNMPC 100  
Db 42 MCEPFTGFVVKDCQDRTA---AQCDCIPGTSFSPDYHTRPHCESCRHNSGFLIRN--C 96  
Qy 101 SSLPRVLCTC-----C--SRCLEC-----MLSIIFPOLPPQTOL 131  
Db 97 TVTNAECSCSKMWCQDOECTEDPLNLPALTRQPSPTSPSPPPPHL 145

RESULT 8  
GYHU  
granulin precursor [validated] - human  
N;Alternate names: epithelin  
N;Contains: granulin A; granulin B; granulin C; granulin D; granulin E; granulin F; gran  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1992 #sequence\_revision 03-May-1996 #text\_change 31-Dec-2004  
C;Accession: JCI284; A38128; A38118; A36698; B36698; C36698; D36698; A56873  
R;Bhandari, V.; Bateman, A.  
Biochem. Biophys. Res. Commun. 188, 57-63, 1992  
A;Title: Structure and chromosomal location of the human granulin gene.  
A;Reference number: JCI284; MUID:93038704; PMID:1417868  
A;Accession: JCI284  
A;Molecule type: DNA  
A;Residues: 1-593 <SHA>  
A;Cross-references: UNIPROT:P28799; UNIPROT:Q9UCH0; UNIPARC:UPI00000015E0  
R;Florman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Todaro, G.J.  
J. Biol. Chem. 267, 13073-13078, 1992  
A;Title: The epithelin precursor encodes two proteins with opposing activities on epithel  
A;Reference number: A38128; MUID:92317004; PMID:1618805  
A;Accession: A38128  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-593 <PLO>  
A;Cross-references: UNIPARC:UPI00000015E0; GB:X62320; NID:G31192; PIDN:CAA44196.1; PID:9  
R;Bhandari, V.; Palfree, R.G.E.; Bateman, A.  
Proc. Natl. Acad. Sci. U.S.A. 89, 1715-1719, 1992  
A;Title: Isolation and sequence of the granulin precursor cDNA from human bone marrow rev  
A;Reference number: A38118; MUID:92179253; PMID:1542665  
A;Accession: A38118  
A;Molecule type: mRNA  
A;Residues: 1-406, 'R', 408-433, 'G', 435-453, 'G', 455-459, 'Q', 461-546, 'A', 548-566, 'R', 568-59  
A;Cross-references: UNIPARC:UPI0000151BFF; GB:W75161; NID:G183612; PIDN:AA58617.1; PID:  
A;Note: this sequence has been revised in reference JCI284  
R;Bateman, A.; Belcourt, D.; Bennett, H.; Lazure, C.; Solomon, S.

Biochem. Biophys. Res. Commun. 173, 1161-1168, 1990

A;Title: Granulins, a novel class of peptide from leukocytes.

A;Reference number: A36698; MUID:91097544; PMID:2268320

A;Accession: A36698

A;Molecule type: protein

A;Residues: 281-336 <BAT>

A;Cross-references: UNIPARC:UPI000001744F2

A;Note: this protein was purified and characterized as granulin A

A;Accession: B36698

A;Molecule type: protein

A;Residues: 206-218, 'H', 220-233 <BA2>

A;Cross-references: UNIPARC:UPI00001744F3

A;Note: this protein was purified and characterized as granulin B

A;Accession: C36698

A;Molecule type: protein

A;Residues: 364-367, 'X', 369-385, 'H', 387-396 <BA3>

A;Cross-references: UNIPARC:UPI00001744F4

A;Note: this protein was purified and characterized as granulin C

A;Accession: D36698

A;Molecule type: protein

A;Residues: 442-446, 'XDTSS', 456-458, 'DQ', <BA4>

A;Cross-references: UNIPARC:UPI00001744F5

R;Kardana, A.; Bagshawe, K.D.; Coles, B.; Read, D.; Taylor, M.  
Br. J. Cancer 67, 686-692, 1993

A;Title: Characterisation of UGP and its relationship with beta-core fragment.

A;Reference number: A56873; MUID:93229246; PMID:8471426

A;Accession: A56873

A;Molecule type: protein

A;Residues: 281-283, 'X', 285-289, 'S', 291-295 <KAR>

A;Cross-references: UNIPARC:UPI0000070B1B

A;Experimental source: urine

A;Note: sequence extracted from NCBI backbone (NCBIF:129524)

C;Genetics:

A;Gene: GDB:GRN

A;Cross-references: GDB:I36006; OMIM:138945

A;Map position: 1pter-1qter

A;Intons: 46/3; 88/3; 117/1; 154/3; 200/1; 236/3; 279/1; 311/3; 393/3; 471/3; 548/3

C;Keywords: glycoprotein; tandem repeat

F;1-17/Domains: signal sequence #status predicted <SIG>

F;18-593/Product: granulin #status predicted <MAT>

F;18-593/Product: progranulin #status predicted <PRO>

F;18-44/Product: pargranulin #status experimental <PGR>

F;58-113/Product: pargranulin G #status predicted <GRG>

F;123-179/Product: granulin F #status predicted <GRF>

F;206-261/Product: granulin B #status experimental <GRB>

F;281-336/Product: granulin A #status experimental <GRA>

F;364-417/Product: granulin C #status experimental <GRC>

F;442-496/Product: granulin D #status predicted <GRD>

F;518-573/Product: granulin E #status predicted <GRE>

F;368/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 10.0%; Score 80.5; DB 1; Length 593;  
Best Local Similarity 24.2%; Pred. No. 8.4;  
Matches 31; Conservative 16; Mismatches 64; Indels 17; Gaps 6;

Qy 3 SCPEE----QYWAALLGTCMFCKALCNHQSQRTCAASCGEFWDLSPGDVITPNACPOST 58  
||| :  
Db 289 SCPDGYTCCRLOSGAWGCCPTQAVCCEDH1HCCEPA--GFTCDTKGTCEOGPHQVPWME 346  
||| :  
Qy 59 LWP-HSOVAERMAGGDVQCQG--TSYPSTFLLLWPHCLLSVSNMPCSSLPRVLCT-----C 110  
||| :  
Db 347 KAPAHLSLPDPQALKRDVPDCNVSCPSDDTC---CQLTSGEWGGCPPEAVCCSDQHHC 403  
||| :  
Qy 111 CSRCLECM 118  
||| :  
Db 404 CPQGYTVCY 411  
||| :

C;Accession: T43457  
R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, December 1999  
A;Reference number: Z22517  
A;Accession: T43457  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-349 <AAA>  
A;Cross-references: UNIPROT:Q9UF43; UNIPARC:UIP0000072EF6; EMBL:AL133619  
A;Experimental source: adult testis; clone DKFZp434Ez321  
C;Genetics:  
A;Note: DKFZp434Ez321.1

Query Match            10.0%; Score 80; DB 2; Length 349;  
Best Local Similarity   25.9%; Pred. No. 5.9;  
Matches   38; Conservative   13; Mismatches   46; Indels   50; Gaps   9;

Qy     10 WAALLGTF-----CMFKCAICN----HQSQRTCAASCGEF----- 39  
      |||:|||: |||: |  
Db     70 WAATMGTKGSRVLPFCPLSKALPHDPDSGPHPAODSGLWSRAHFPLSLGLTSGGHLTG 129  
      |||:|||: |||: |

Qy     40 -WLSFGDSVITPNACQSTLWPHSQVAERWAGDV--QCQTSPYSIFLLWPHCLLSVS 96  
      |||:|||: |||: |

Db     130 GWS-QPGN---IVAGAVPRAL--PSORDMENGVGGFPFSRCGN---SSSELFWAKCGPSRQ 181  
      |||:|||: |||: |

Qy     97 NMPCSS-----LPRVLCTCCSRC 114  
      |||:|||: |

Db     182 PQPCSAGDADTREAMLTLGTCCSMC 208  
      |||:|||: |

RESULT 10  
S08167  
Balbian ring 3 protein - midge (Chironomus tentans)  
C;Species: Chironomus tentans  
C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Aug-2004  
C;Accession: S08167  
R;Paulsson, G.; Lendahl, U.; Galli, J.; Ericson, C.; Wieslander, L.  
J. Mol. Biol. 211, 331-349, 1990  
A;Title: The balbian ring 3 gene in Chironomus tentans has a diverged repetitive structure  
A;Reference number: S08167; MUID:90172404; PMID:1689777  
A;Accession: S08167  
A;Status: not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-1700 <PAU>  
A;Cross-references: UNIPROT:Q03376; UNIPARC:UIP0000126788; GB:X52263; NID:g7057; PIDN:CMAN  
C;Genetics:  
A;Gene: BR3  
A;Map position: 4

Query Match            9.9%; Score 79.5; DB 2; Length 1700;  
Best Local Similarity   26.0%; Pred. No. 25;  
Matches   39; Conservative   15; Mismatches   47; Indels   49; Gaps   11;

Qy     3 SCP-EEQVWAALLGTCMFCKAIC-NHQSQRCAASCGEFDLSPGD-SVIT----- 50  
      |||:|||: |||: |

Db     818 ACPNKQCKAPLVWSDEFCDVCNPASAMKTC-----LSPKEWNKVTTCTDCNCPPK 868  
      |||:|||: |||: |

Qy     51 PNACQSTLWPHSQV-----AEERMAGG----DVQCQTSPYSTFL-----LWP-----H 90  
      |||:|||: |||: |

Db     869 PDCCPGTGKWMDDKCKCGCPNAQTDCAGKKGFNDFTCSGCPCSGKLDTGTNTKWSAETCT 928  
      |||:|||: |||: |

Qy     91 CLLSVSNMPCSSLPRV---LCTCCSRCLEC 117  
      |||:|||: |||: |

Db     929 CGCGDVNRNCGNLKNFNLDLCQ-----EC 953  
      |||:|||: |||: |

RESULT 11  
JE0095  
gastric mucin MUC5AC precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 22-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C;Accession: JE0095  
R;van de Bovenkamp, J.H.B.; Hau, C.M.; Strous, G.J.A.M.; Bueller, H.A.; Dekker, J.; Einer-

RESULT 9  
T43457  
hypothetical protein DKFZp434E2321.1 - human (fragment)  
C/Spectes: Homo sapiens (man)  
C/Date: 21-Jan-2000 #sequence revision 21-Jan-2000 #text change 09-Jul-2004

Biochem. Biophys. Res. Commun. 245, 853-859, 1998  
A:Title: Molecular cloning of human gastric mucin MUC5AC reveals conserved cysteine-rich  
A:Reference number: JE0095; MUID:98249803; PMID:9586204  
A:Accession: JE0095  
A:Molecule type: mRNA  
A:Residues: 1-1373 <BOV>  
A:Cross-references: UNIPROT:O75372; UNIPARC:UPI000017C12D; GB:AF043909  
A:Experimental source: stomach  
E:1-19/Domain: signal sequence #status predicted <SIG>  
F:273-300/Domain: leucine zipper #status predicted <L2P>

Query Match 9.8%; Score 78.5; DB 2; Length 1373;  
Best Local Similarity 22.8%; Pred. No. 26;  
Matches 39; Conservative 14; Mismatches 53; Indels 65; Gaps 11;  
Qy 8 QYWAALL-----GT-----CMFKCAINHQSQRTCAA-----SCGE--- 38  
Db 630 QHWCSQLTDAGPFGCHAAVKPGTYTYSNCFDTCNCRSESDCLCAALSSVYHACAAGV 689  
Qy 39 ---FMDLSPGDSVITP--NACPQSTLWPHSOVAE-----ERMAGDVQCGTSY----- 81  
Db 690 QLGW-----RDGCTKPMWTCPKSMY-HYHVSCTQPTCRSLSGDITCSVGFIPVDGCI 744  
Qy 82 --PSTFLWPHCLLSVNMPC-----SSLPR-----VLCTCCSRCLCQM 118  
Db 745 CPKGTFLDDTKCKVQASNCPCYHRGSMIPNGESVHDSGAICTCTHGLKLCI 795

RESULT 12  
T27684  
hypothetical protein ZK1067.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
A:Accession: T27684  
R:Thomas, K.  
submitted to the EMBL Data Library, March 1996  
A:Reference number: Z20404  
A:Accession: T27684  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-2219 <WIL>  
A:Cross-references: UNIPROT:Q23388; UNIPARC:UPI00000761CD; EMBL:Z70038; PIDN:CAA93884.1.  
A:Experimental source: clone ZK1067  
C:Genetics:  
A:Gene: CESP:ZK1067.2  
A:Map position: 2  
A:Introns: 139/3; 246/3; 487/3; 784/1; 960/2; 1067/3; 1113/3; 1171/3; 1321/2; 1383/3; 14

Query Match 9.7%; Score 77.5; DB 2; Length 2219;  
Best Local Similarity 20.9%; Pred. No. 48;  
Matches 31; Conservative 16; Mismatches 44; Indels 57; Gaps 7;  
Qy 2 RSCPEQYWAALLGTCMF-----CGSLYVEVTLDCGHRITTPCSRINSKQDSCTKLLCGH---C-KAICNHQSQRTC 32  
Db 1577 KACVEE-----CGSLYVEVTLDCGHRITTPCSRINSKQDSCTKLLCGH---AC 1626  
Qy 33 AASCGEFDLSPGDSVIT--PNACPQSTLWPHSOVAERMAGDVQCGTSYPSTFLWPH 90  
Db 1627 AAKCGEFTLVSECSQLVGMPFLSCGHIKQLTCSKISANEI---DLTCDQRCETMLACPH 1683  
Qy 91 CLLSVSNMPCSSLPVLCTCCSRCLCQM 118  
Db 1684 KCAEICQPCT-----VECM 1698

RESULT 13  
S51604  
receptor-like tyrosine kinase Etk-1 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 29-May-1998  
A:Accession: S51604  
R:Maisonpierre, P.C.; Barrezaeta, N.X.; Yancopoulos, G.D.  
Oncogene 8, 3277-3288, 1993

A:Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam  
A:Reference number: S49015; MUID:94067777; PMID:7504232  
A:Accession: S51604  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-981 <MAI>  
A:Cross-references: UNIPARC:UPI0000175666; EMBL:S68029  
A:Note: the authors translated the codon GAC for residue 170 as Glu  
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h  
E:1-19/Domain: protein kinase homology <KIN>  
F:651-917/Domain: protein kinase homology <KIN>  
F:659-667/Region: protein kinase ATP-binding motif

Query Match 9.6%; Score 77; DB 2; Length 981;  
Best Local Similarity 26.5%; Pred. No. 26;  
Matches 36; Conservative 7; Mismatches 61; Indels 32; Gaps 8;  
Qy 4 CPBEQYWAALLGTCMFCKAICNHQSQRTCAASCGEFDLSPGDSVITPNACPOSTLWPHS 63  
Db 278 CSAEGEWLVPIGKCM-CKA-GYEEKNGTCQVCRPGFFKASPHSQ--TCSKCP-----PHS 328  
Qy 64 QVAERMGAGDVQCGTSY-----PSTFLWPHCLLSVSNMPCSSLPVLCTCCSRCLC 117  
Db 329 YTHEE--ASTSCVCEKDYFRRESDPPT-----MACTRPPSAPRNAISVNYE- 372  
Qy 118 MLSIIFPQPTQLSG 133  
Db 373 -TSVFLEWIPPADTGG 387

RESULT 14  
S49015  
receptor tyrosine kinase Etk-1 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
A:Accession: S49015; S51602  
R:Maisonpierre, P.C.; Barrezaeta, N.X.; Yancopoulos, G.D.  
Oncogene 8, 3277-3288, 1993  
A:Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam  
A:Reference number: S49015; MUID:94067777; PMID:7504232  
A:Accession: S49015  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1005 <MAI>  
A:Cross-references: UNIPROT:P54757; UNIPARC:UPI0000050E8; EMBL:S68024  
A:Note: the authors translated the codon GAC for residue 170 as Glu  
A:Accession: S51602  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-305, 'G', 359-1005 <MA2>  
A:Cross-references: UNIPARC:UPI0000175665; EMBL:S68026  
A:Note: the authors translated the codon GAC for residue 170 as Glu  
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h  
E:675-941/Domain: protein kinase homology <KIN>  
F:683-691/Region: protein kinase ATP-binding motif

Query Match 9.6%; Score 77; DB 2; Length 1005;  
Best Local Similarity 26.5%; Pred. No. 27;  
Matches 36; Conservative 7; Mismatches 61; Indels 32; Gaps 8;  
Qy 4 CPBEQYWAALLGTCMFCKAICNHQSQRTCAASCGEFDLSPGDSVITPNACPOSTLWPHS 63  
Db 278 CSAEGEWLVPIGKCM-CKA-GYEEKNGTCQVCRPGFFKASPHSQ--TCSKCP-----PHS 328  
Qy 64 QVAERMGAGDVQCGTSY-----PSTFLWPHCLLSVSNMPCSSLPVLCTCCSRCLC 117  
Db 329 YTHEE--ASTSCVCEKDYFRRESDPPT-----MACTRPPSAPRNAISVNYE- 372  
Qy 118 MLSIIFPQPTQLSG 133  
Db 373 -TSVFLEWIPPADTGG 387

RESULT 15  
E64445  
polyferredoxin 4x2[4Fe-4S] fwdF - Methanococcus jannaschii  
N/Alternate names: formylmethanofuran dehydrogenase (tungsten) chain F [misnomer]  
C/Species: Methanococcus jannaschii  
C/Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 05-Oct-2004  
C/Accession: E64445  
R/Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Xson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.  
Science 273, 1058-1073, 1996  
A/Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.  
A/Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii  
A/Reference number: A64300; MUID:96337999; PMID:8688087  
A/Accession: E64445  
A/Status: nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-355 <BUL>  
A/Cross-references: UNIPROT:Q58566; UNIPARC:UPI0000066ADC; GB:U67558; GB:L77117; NID:gl5  
C/Genetics:  
A/Map position: FOR1106732-1107799  
A/Suprafamily: formylmethanofuran dehydrogenase, subunit F;ferredoxin 2[4Fe-4S] homolog  
C/Keywords: 4Fe-4S; iron-sulfur protein; metalloprotein  
F/109-174/Domain:ferredoxin 2[4Fe-4S] homology <FER3>  
F/33,36,39,83/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted  
F/43,73,76,79/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted  
F/117,120,123,166/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted  
F/127,156,159,162/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted  
F/136,139,202,254/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted  
F/206,244,247,250/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted  
F/276,279,282,323/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted  
F/286,313,316,319/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 9.5% Score 76.5; DB 2; Length 355;  
Best Local Similarity 20.8%; Pred. No. 12;  
Matches 30; Conservative 20; Mismatches 45; Indels 49; Gaps 8;  
Qy 17 CMFCKA---ICNHOSQRTCAASC-----GEFWDLSPGDSVITPNACPQ----STLWP 61  
Db 196 CVFCKVCFVCPHDAIEVICYKCPMKRIPQAKLYEDI TGTVIDKDACVTCGWCAFI 255  
Qy 62 HSQVAERRMAGGDV-----QCGTSPSTFLLWPHCLLSVSNMPCSSL-----P 104  
Db 256 AEAIEVEKPFKGLIIDVNACNA-----CGACISITCPCSALEFPKPKDAEKVP 304  
Qy 105 RV-----LCTCCSRCLC-CMLSII 122  
Db 305 RIIVNQNLVLCGACAKACPVNAI 328

Search completed: December 20, 2005, 10:43:31  
Job time : 41 secs